

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 09:17:11; Search time 4372 Seconds
(without alignments)
10163.182 Million cell updates/sec

Title: US-10-690-246A-1

Perfect score: 1 acgcggagatagtaggaag.....ttttgtttgtttttcgg 917

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	910	99.2	910	AY378149	AY378149 Phalaenop
2	359.4	35.2	1030	AY378148	AY378148 Phalaenop
3	339.2	37.0	942	AY196350	AY196350 Oncidium
4	335	36.5	952	AB094964	AB094964 Asparagus
5	324.2	35.4	1028	AY378147	AY378147 Phalaenop
6	316.8	34.5	980	AY378150	AY378150 Phalaenop
7	304.2	33.6	1005	AB071378	AB071378 Lilium re
8	299.4	32.6	1039	AF503913	AF503913 Lilium lo
9	295.6	32.2	833	AF209729	AF209729 Hemerocal
10	292.8	31.9	938	AF230706	AF230706 Tacca cha
11	285.4	31.1	651	AY337750	AY337750 Eupomati
12	283.4	31.1	651	AY337751	AY337751 Eupomati
13	284.8	31.1	852	AB050649	AB050649 Magnolia
14	282.6	30.8	830	AY621154	AY621154 Alpinia h
15	282.2	30.8	1002	AB094965	AB094965 Tulipa ge
16	265.8	29.0	1016	AB094966	AB094966 Tulipa ge
17	264.4	28.8	830	AY397762	AY397762 Chloranth
18	263	28.7	1084	AB003323	AB003323 Oryza sat
19	263	28.7	1210	AK069317	AK069317 Oryza sat

20	261	28.5	896	8	AY627630	AY627630 Akebia tr
21	260	28.4	1061	8	AF077760	AF077760 Oryza sat
22	259	28.2	768	8	AY436722	AY436722 Drimys wi
23	256.2	27.9	851	8	AY436723	AY436723 Drimys wi
24	255.4	27.9	810	8	AY436725	AY436725 Drimys wi
25	254.4	27.7	1008	8	AF052874	AF052874 Papaver n
26	254.2	27.7	1166	8	AY541065	AY541065 Hordeum v
27	253	27.6	809	8	AY436724	AY436724 Drimys wi
28	253	27.6	828	8	ACAA19959	AA19959 Acanthace
29	251	27.4	959	8	AB007506	AB007506 Acanthace
30	247.4	27.0	834	8	ACAA19955	AA19955 Acanthace
31	245.8	26.8	852	8	AY436715	AY436715 Saruma he
32	239.4	26.1	906	8	GHY9724	GHY9724 Gerbera h
33	239.4	26.1	958	8	AY627631	AY627631 Akebia tr
34	238.6	26.0	643	8	TAB57737	TAB57737 Trifolium
35	238.6	26.0	1083	8	AB107993	AB107993 Trifolium
36	238.4	26.0	935	8	AY436736	AY436736 Lindera e
37	236	25.7	1257	6	CO855034	CO855034 Sequence
38	236	25.7	1257	6	AX478035	AX478035 Sequence
39	235	25.6	1004	8	AF230697	AF230697 Asarum eu
40	233.4	25.5	810	8	AY337748	AY337748 Persea am
41	231.4	25.2	603	8	AY162881	AY162881 Platanus
42	229.8	25.1	763	8	AY162881	AY162881 Platanus
43	228	24.9	946	6	AR372458	AR372458 Sequence
44	227.2	24.8	681	6	AR372459	AR372459 Sequence
45	226.8	24.7	755	8	AF230699	AF230699 Calycanth

ALIGNMENTS

RESULT 1	AY378149	910 bp	mrna	linear	PLN 09-AUG-2004
LOCUS	Phalaenopsis equestris MADS box transcription factor (MADS2) mRNA,				
DEFINITION	complete cds.				
ACCESSION	AY378149				
VERSION	AY378149.1 GI:38680584				
KEYWORDS	Phalaenopsis equestris				
SOURCE	Phalaenopsis equestris				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; higher Epidendroideae; Vandaceae; Aeridinae; Phalaenopsis.				
REFERENCE	1 (bases 1 to 910)				
AUTHORS	Tsai,W.C., Kuo,H.C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.				
TITLE	Four DBF-like MADS Box Genes Displayed Distinct Floral Morphogenetic Roles in Phalaenopsis Orchid Plant Cell Physiol. 45 (7), 831-844 (2004)				
JOURNAL	Plant Cell Physiol. 45 (7), 831-844 (2004)				
PUBMED	15295066				
REFERENCES	2 (bases 1 to 910)				
AUTHORS	Tsai,W.C., Chen,W.H. and Chen,H.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-SRP-2003) Department of Biology, National Cheng Kung University, 1 University Rd., Tainan, Taiwan 701, Republic of China				
FEATURES	Location/Qualifiers				
SOURCE	1..910				
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	/note="PcMADS2"				
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	/db_xref="GI:38680585"				
	/translation="MGRGKIKIKIENPTNRQVTSKRRVILKKAKELIVLCDAQVS LIMFSSTCKLADYCSPTDIDKIGIERVQVVTGMDLMMNQYERMONTLKLHLEINQNL"				

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 Qy 423 GGCATTAAGCAATCGCGCGCTCTTGAAGCAAACTTTGAAAGAGCTCTTGAATTTGTAAG 482
 Db 602 GGGCGTTAAAGAGCTGCGCGCTCTTGAAGCAAAATTTGAGAGAGCTCGTTAAGATTTGCG 661
 Qy 483 GCATAGAAAGTATCATGTGATCGCCACACAAATCGACATTCACAGAAAAAGCTTAAAG 542
 Db 662 GCAGAGAAAGTATCATGTGATCGCTACGCAAAACAGACATTCGACAGAAAAAGCTCAAAAG 721
 Qy 543 CACAGAGAAACTTACCGCGCTCTTAATACATGAATCTGATP---TGAAAGAGAGAAATCC 599
 Db 722 CAGCAGACAATATATACAGAGCCCTTACGCAATGCACTGAGAGAGCTGAGAGAGAAATCA 781
 Qy 600 GAATGAGGTTTAAATGTAAGAAACAGAGTAAATTTATGAAATTCGATTCGAATGT 659
 Db 782 ACCGTGCAAGTTTCTCTGTAAGATCTTAAGCTGCAATCTATGACAGCTCAATCTCATGCG 841
 Qy 660 GAATGAGTGTCTCAGAG 676
 Db 842 AATCGGCTGCACCGGA 858

RESULT 3
 AY196350 942 bp mRNA linear PLAN 02-MAR-2003
 LOCUS Oncidium cv. 'Gower Ramsey' MADS box protein (MADS3) mRNA, complete
 DEFINITION cds.
 ACCESSION AY196350
 VERSION AY196350.1 GI:28630894
 KEYWORDS
 SOURCE
 ORGANISM
 .
 Oncidium cv. 'Gower Ramsey',
 Oncidium cv. 'Gower Ramsey',
 Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 Epidendroideae; higher Epidendroideae; Maxillarieae; Oncidiinae;
 Oncidium.
 1 (bases 1 to 942)
 Hsu, H.-F. and Yang, C.-H.
 An Orchid (Oncidium Gower Ramsey) Ap3-like MADS Gene Regulates
 Floral Formation and Initiation
 Plant Cell Physiol. 43 (10), 1198-1209 (2002)
 JOURNAL 22294943
 MEDLINE 12407200
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 1. .942
 /organism="Oncidium cv. 'Gower Ramsey'"
 /mol_type="mRNA"
 /cultivar="Gower Ramsey"
 /db_xref="taxon:96474"
 1. .942
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 /note="OMADS3"
 121. .735
 /gene="MADS3"
 /note="similar to Ap3"
 /codon_start=1
 /product="MADS box protein"
 /protein_id="AA045824.1"
 /db_xref="GI:28630895"
 /translation="MGRGKIEIKIENPTSRQVYSKRLGITTKAMELTVLCAKVS
 LIMFSSGSLSDYCSPTSEIKDAPORQOVTFDIDIAQYOMSGTLMNLRVNHKLQ
 MEIRKQENLEGLDYKEIRGLKELESIKIVRRKRVIVATQDTYKKKLSRTREM
 YPALNLEQVDDENQKSFIAEDLSGYNSAISANQRLAHCL"

ORIGIN

Query Match 37.0%; Score 339.2; DB 8; Length 942;
 Best Local Similarity 74.0%; Pred. No. 1e-67;
 Matches 444; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

Qy 72 AGAGATGGGAGGGGAGAGATAGATTAATAAAGATAGAAATCCAGCAACGCAAGT 131
 Db 117 AGCAATGGGAGAGGAAAGATAGATTAATAAAGATAGAAATCCAGCAACGCAAGT 176
 Qy 132 TACATATTTAAGAGAGAGTTGGATATCTGAAGAAAGCCAGAGACTCATCTGTCG 191
 Db 177 AACTTACTCAAAAGAGCGACTTGAAATTAACGAAAAAGCCATGAAATTAACAGTGCCTG 236
 Qy 192 TGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGAGCTGATTAAGTCA 251
 Db 237 CGAGGCTAAGGTTTCTCTCATCATGTTCTCAAGCTCTGGCAATTAATCTGATTAAGTCA 296
 Qy 252 CCCCTACTGATATTAAGGGATATATGAGAGTACAGAGTGTGATCTGAAATGATCT 311
 Db 297 CCTTCTACGAATTAATAAGATGCGTTTCAAGGTATCAGCAAGTTACCGGCTTGAATAT 356
 Qy 312 ATGGAATGCTCAGTATGAGAGATGCAATACGCTGAGAGATCTGAATGATTAACCA 371
 Db 357 CTGGAGTCCCAATACAGAGAGATGCAAGTACTGATGATTAATCTCAGAGAGTTATCA 416
 Qy 372 AAACCTGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 431
 Db 417 TAACTTCAATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 476
 Qy 432 GCACTGCGCGGCTCTTGAAGCAAACTTTGAAGAGTCTTGAATTTGAGCATAGAAA 491
 Db 477 GGAATCGCGCGCTTCTGACGAAATTTGAAGAGTGAATTAAGTCTTGGGAGAGAAA 536
 Qy 492 GTATCATGTATGCGCACACAACTGACACTTACAGAAAAAGTTAAAGCACAAAGGA 551
 Db 537 GTATCATGTATGCGCTACGCAACAGACACTTACAGAAAAAGTTAAAGCACAAAGGA 596
 Qy 552 AACTTACCGGCTCTTATACATGACT---GGAATGAAAGAGAGAAATCGAATCAAG 608
 Db 597 AATGTACCGAGCCCTTATGATGAGCTGACAGAGAGTGAATGAGAAATCAACAGCGCAG 656
 Qy 609 TTTTATGTAGAAACAGAGTAAATTTTGAATTTGAAATTCGATTCGAAATGTAAGTG 668
 Db 657 TTTTATGTAGAAATCTTACGCGGTGCTCAACAGGCAATCAATGCGGAGATCAAGAG 716

RESULT 4
 AB094964 952 bp mRNA linear PLAN 29-APR-2003
 LOCUS Asparagus officinalis AODEF mRNA for MADS-box transcription factor,
 DEFINITION complete cds.
 ACCESSION AB094964
 VERSION AB094964.1 GI:30172218
 KEYWORDS
 SOURCE
 ORGANISM
 .
 Asparagus officinalis (garden asparagus)
 Asparagus officinalis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 Asparagaceae; Asparagus.
 1
 Park, J., Ishikawa, Y., Yoshida, R., Kanno, A. and Kameya, T.
 Expression of AODEF, a B-functional MADS-box gene, in stamens and
 inner tepals of dioecious species Asparagus officinalis L
 Plant Mol. Biol. (2002) in press
 2 (bases 1 to 952)
 Kanno, A.
 Direct Submission
 Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
 School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
 980-8577, Japan (E-mail: kanno@life.tohoku.ac.jp, Tel: 81-22-217-5725,
 Fax: 81-22-217-5725)
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 1. .952
 /organism="Asparagus officinalis"

Oy		374	ACCTGAGGAAGAATATTAGAGGGAAAGGAGGAATTGAGGGCATGACAATAAAGC	433
Dd		506	ATCTGAGAGGGAAGTAAAGCAAGAGATGGCGGAAGACTTTGAGGCATGTGATTCAGG	565
Oy		434	AAGTGCCGGCTCTTAGCAAACTTTGGAAAGTCTTTAGATTGSCATPAAAAAT	493
Oy		494	ATCATGTGATGCCAACAAAATTAACAATTGAAGAAAAAGCTTAAAGCAAAGGAAA	553
Dd		566	AAGTGCCGGCTCTTAGCAAAACATTTAGTAGGCAATTGAAAGCTPAGTACGAAATAGAAAT	625
Oy		626	ATCATGTGATTCAGTACCAGCGCACCTPAAGAAAGAAAGTTGAAGAACTCCAMGAAA	685
Oy		554	CTTACCGCGCTCAATACATGAACTGATATGAAGAGAGAAATCCGAACCTACGGTTTTA	613
Dd		686	CACACCGGAACCTTAATGACAGAAATTGAAAATCGTTGAGAGACACCAGTGTATGGTTCC	745
Oy		614	ATGTAGAAAACACAGAGTAGAATTATAGMAAATTGCAATTCCAATGTGATGATGTCTTC	673
Dd		746	ACG-----AGAAITTAAGCAATTATAGAGGGTGTTTGCTCTTGCAAAATGACGGGCTTC	799
Oy		674	AGATGTTTTCTTTAGGGTTGTTCATCCGATACGCCAANTCGCTTGTGATTAGGTTATG	733
Dd		800	ACATGTAGTACCTTCGCG---GTGAAACCCCAACCAAAANCTTCAAGAAACGGAGATATA	856
Oy		734	AATCAGATGATCTTAGCTTCATTAAT	760
Dd		857	GCTCTCACGATCTTCGCTCGCTTGAT	883
RESULT_6				
AY378150		980 bp	mRNA linear	PIN 09-AUG-2004
LOCUS				
DEFINITION			Phalaenopsis equestris MADS box transcription factor (MADS) mRNA,	
ACCESSION			complete cds.	
VERSION			AY378150	
KEYWORDS			AY378150.1 GI:38680586	
SOURCE				
ORGANISM			. Phalaenopsis equestris Phalaenopsis equestris Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epiphytrodeseae; higher Epidendroideae; Vandeeae; Aeridiinae;	
REFERENCE				
AUTHORS			Teai,W.C., Kuoh,C.S., Chuang,M.H., Chen,W.H. and Chen,H.H. Four DEF-like MADS Box Genes Displayed Distinct Floral Morphogenetic Roles in Phalaenopsis Orchid Plant Cell Physiol. 45 (7), 831-844 (2004)	
JOURNAL			15295066	
PUBMED			(bases 1 to 980) 2 (bases 1 to 980)	
REFERENCES			Teai,W.C., Chen,W.H. and Chen,H.H. Direct Submission Submitted (02-SEP-2003) Department of Biology, National Cheng Kung University, 1 University Rd., Tainan, Taiwan 701, Republic of China	
TITLE			Location/Qualifiers	
JOURNAL			1.. 980	
FEATURES			/organism="Phalaenopsis equestris"	
source			/mol_type="mRNA" /db_xref="taxon:78828" /feature_type="Flower bud" 1.. 980 /gene="MADJ3" /note="PeMADJ3" 196.. 864 /gene="MADJ3" /protein_start=1 /product="MADS box transcription factor" /db_xref="GI:38680587" /translational="MGKGLIKLLENPNQVYSKRRAIGMKASLTLYICDAQLS LMVFSTGFSEYCSPTDTTKSVYRQQVSINSMSQYEIMQTTLHLKEIHNNLE RIIRRMGEIDLGLBIKLRLGLEONMDALKLVNRKKHYHIVISTQTDPRKKLKNSQET	
gene				
CDS				

ORIGIN	Query Match	34.5%;	Score 316.8;	DB 8;	Length 980;
	Best Local Similarity	65.3%;	Pred. No.1,5e-62;		
	Matches 503;	Conservative 0;	Mismatches 252;	Indels 15;	Gaps 2;
QY	65	GGAAGAGAGAGATGGGAGGGGAGAGATAGATATAAAAAAGATAGAGATCCGACGACCA	124		
DB	185	GAAAGAGAACCATGGGAGGGGGAGATCAAGATTAAGAAATTGGAACCCCTACAAACA	244		
QY	125	GGCAAGTTACATATTTCTAAGAGAGAGATTGGGATCTGGAAGAGGCCAAGAGCTCACTG	184		
DB	245	GGCAGGTTACTTACTCTTAAGAGAGGGGCTGGAGATCATGAAAAAGCGAGAGCTCAAG	304		
QY	185	TTCTCTGATGATCTCAGAGTCTCTCATCATGTTCTTCACACAGCAAGAAAGTTGGCTGATT	244		
DB	305	TTCTCTGATGATGCTCACTCTCTCTCTTGTATGTTCTTCACACACCGGCAAGTTCTCCGAGT	364		
QY	245	ACTGCAAGCCCTTACTGATATTAAAGGGAATATATGAGAGTACAGGTTGTGACTGGA	304		
DB	365	ATTGATGCTTACACACGATACCAAGATGATATGATTCCTTACCAAGAGGTGCTCCGCA	424		
QY	305	TGGAATCTATGAAATGCTCAGATATGAGAGAGATGCAAGATTAAGCTGAGACATCTGAATGAGA	364		
DB	425	TAAATTTATATGAGAGGACAGATACAGAAAGATGCAAGATTAAGCTGAAATCTTGAAGAGCA	484		
QY	365	TTAACCAAAAACCTGAGGAAGAGATTTAGAGAGGAAGAGGGGAGGAATTTGAGGGCATGCG	424		
DB	485	TAAACCAAACTTTAGAGAGAGAGATTAAGCAGAGAGATGGGGAGAGATCTTGAAGGGCTAG	544		
QY	425	ACATTAAGCAACTGCGCGGCTTTGAGCAAACTTTGGAAGAGTCTCTTAAGATTGTTAGGC	484		
DB	545	AAATCAAGAGACTGGTGCTCTTGAACAAATATGACAGAGCCCTTAAGCTTGAAGGA	604		
QY	485	ATAGAAAGATCATATGATGCTGCCACCAAACTGACATTTCAAAAGAGCTTAAAGCA	544		
DB	605	ATCGAAGATATCACTCATATGACACCCAGACAGATTAATCAAAAAAGTTGAAAAAATCT	664		
QY	545	CAAGGGAAGACTTACCGGCTCTAATATACATGAACTGATATGAAAGAGAGAAATCCGAAT	604		
DB	665	CTCAAGAAACCCACAGAACTTACTCCGGAGCT-----GGAAACTGAGACG	712		
QY	605	ACGGTTTAAATGTAGAAAAACAGATAGAAATTTAAGAAATTCATTCATGCTGAATG	664		
DB	713	CCGTCTACATAGTGATGATATCAAAACAATATGATGCGCGCTTGCACTTGAAGATG	772		
QY	665	AGTGTCTCAGATGTTTCTCTTATAGGGTGTTCATCCGAATCAACCCCAATGCTGTGTT	724		
DB	773	GGGCTTCTTCACTTGATTCATTTTGG---TACCACAAACAGCCAGCCGAACCTTCAAGSAG	829		
QY	725	TAGGTTATGAATCACATGATCTTAGCCTTGATATGAGAGAGATATATATGATTTTATTT	784		
DB	830	TTGGAATATGCTCTTATATATCTAGCTCTCGCTGATCTTTATATATCTGATGCCAATG	889		
QY	785	GTAATTTTATTTATGTTTGAACCTTGAATTTATGAGATGGGGATCTA	834		
DB	890	CTTAATTTATATCTATGATCTGATGATGTTCTTACGCTTACAAGTAGGGCTCA	939		
RESULT 7	AB071378	1005 bp	mRNA	linear	PLN 09-MAY-2002
LOCUS	AB071378				
DEFINITION	Lilium regale LRDEF	MRNA for MADS-box transcription factor,			
ACCESSION	AB071378				
VERSION	AB071378.1	GI:20513259			
KEYWORDS					
SOURCE	Lilium regale				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;				

REFERENCE 1
AUTHORS Winter, K. U., Weiser, C., Kaufmann, K., Bohne, A., Kirchner, C.,
TITLE Kanno, A., Saedler, H. and Theissen, G.
JOURNAL Evolution of class B floral homeotic proteins: obligate
MEDLINE heterodimerization originated from homodimerization
PUBMED Mol. Biol. Evol. 19 (5), 587-596 (2002)
21959322
2 (bases 1 to 1005)
REFERENCE Kanno, A., Bohne, A., Saedler, H. and Theissen, G.
AUTHORS Direct Submission
JOURNAL Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail: kanno@life.tohoku.ac.jp,
Tel: 81-22-217-5725 (ex. 5725), Fax: 81-22-217-5725)
Location/Qualifiers
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10. .696
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/db_xref="GI:20513260"
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6 AGCATGCGGGCGGGGAAAGATCGAGATTAAAGATGGAAGAACTCGACGATCGACAGGT 65
132 TACATATTCTTAAGAGAGAGATTGGGATCTGGAAGAGCCAGAGAGCTCACTGTTCTG 191
66 CACTTACTCGAAGCGCCGACCGGAATCATCAAGAGGCGACTGACTCATGCTCTG 125
192 TGATGCTCAGGTCCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGAG 251
126 TGATCCGAGGTCTCTCTTCTTATGTTCTTCAGACCGGAAAGCTGTCAAGATTCTGAG 185
252 CCCCTTACTGATATTAAAGGAGATATAGAGGTACAGAGTTGTGACTGGAATGATCT 311
186 CCCCTCAGACAGACGAAAGATCTTCGACCGCTTACAGAGAGCTGTCCGGGATCAACT 245
312 ATGGAATGCTCAGATAGAGAGATGCAAGATACCTGAGATCTGATGATGATTAACA 371
246 CTGAGAGCGCCAAATACAGAAATGCAAAACATTTGAACATCTGAGCGAGATCAACG 305
372 AAACCTGAGAGAGATTAGAGAGAGAAAGGGGAGAAATTGAGAGGCAATGACATAAA 431
306 CAACCTCCGAGAGATCAACCCAGAGATGAGGAGAGAGAGCTGATGATGATGACATCAA 365
432 GCAATGCGCGGCTTTAGAGCAAACTTTGAGAGATCTTTAGATTGTTAGGCAATAGAA 491
366 GGAATGCGGCGCTTTAGAGCAAAATTTGAGAGAGCGCTCAAGCTCGTTGCTACAGAA 425
492 GTATCATGTGATGCCCAACAATGACATTAAAGAAAAGCTTTAAAGACACAGAGGA 551
426 GTATCATGTGATCAACACTCAGACAGAGACTTACAGAAAAGGTCAAAAAATCTCGAAGA 485

ORIGIN

Query Match 33.2%; Score 304.2; DB 8; Length 1005;
Best Local Similarity 68.0%; Pred. No. 1.2e-59;
Matches 474; Conservative 0; Mismatches 208; Indels 15; Gaps 3;

72 AGAGATGGGAGGGGGAAGATAGAGATAAAAAGATAGAGATCCGACGAAACAGCAAGT 131
6 AGCATGCGGGCGGGGAAAGATCGAGATTAAAGATGGAAGAACTCGACGATCGACAGGT 65
132 TACATATTCTTAAGAGAGAGATTGGGATCTGGAAGAGCCAGAGAGCTCACTGTTCTG 191
66 CACTTACTCGAAGCGCCGACCGGAATCATCAAGAGGCGACTGACTCATGCTCTG 125
192 TGATGCTCAGGTCCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGAG 251
126 TGATCCGAGGTCTCTCTTCTTATGTTCTTCAGACCGGAAAGCTGTCAAGATTCTGAG 185
252 CCCCTTACTGATATTAAAGGAGATATAGAGGTACAGAGTTGTGACTGGAATGATCT 311
186 CCCCTCAGACAGACGAAAGATCTTCGACCGCTTACAGAGAGCTGTCCGGGATCAACT 245
312 ATGGAATGCTCAGATAGAGAGATGCAAGATACCTGAGATCTGATGATGATTAACA 371
246 CTGAGAGCGCCAAATACAGAAATGCAAAACATTTGAACATCTGAGCGAGATCAACG 305
372 AAACCTGAGAGAGATTAGAGAGAGAAAGGGGAGAAATTGAGAGGCAATGACATAAA 431
306 CAACCTCCGAGAGATCAACCCAGAGATGAGGAGAGAGAGCTGATGATGATGACATCAA 365
432 GCAATGCGCGGCTTTAGAGCAAACTTTGAGAGATCTTTAGATTGTTAGGCAATAGAA 491
366 GGAATGCGGCGCTTTAGAGCAAAATTTGAGAGAGCGCTCAAGCTCGTTGCTACAGAA 425
492 GTATCATGTGATGCCCAACAATGACATTAAAGAAAAGCTTTAAAGACACAGAGGA 551
426 GTATCATGTGATCAACACTCAGACAGAGACTTACAGAAAAGGTCAAAAAATCTCGAAGA 485

QY 552 AACTTACCGCGCTCTAATACATGAATCTG-----GATATGAAAGAGAGAAATCCGA 602
DB 486 AGCAGCAAGAAAGACTGCTCGTGACCTGGTGAATAGAGATGAAAGATGAAATTCAGT 545
QY 603 CTACGGTTTAAATGATGAAAACAGAGTGAATTTATGAAAATTCGATTCATGTTGA 662
DB 546 CTATGCTT---ATGTGACGAAAGACCCAGCAACTATGATGCGCGCTGCTTGCGGAA 602
QY 663 TGAGTGTCCCTGAGATGTTTCCCTTAGAGGTGTTGATCCGAATCAGCCCAATCTGCTG 722
DB 603 TGGGGCTTCTCATCTGTACAGATTCCG---AGTCAACCGAGCCAGCAAACTGCATG 659
QY 723 TTAGGTTATGATCATCATGATCTTAGCTTCATTA 759
DB 660 GATGGTTATGTTGTTCCAGATCTCCGACTGCGTTGA 696
RESULT 8
AF503913 1039 bp mRNA linear PLN 13-MAY-2002
LOCUS Lilium longiflorum MADS box protein (MADS1) mRNA, complete cds.
DEFINITION AF503913
ACCESSION AF503913 GI:20531752
VERSION AF503913.1
KEYWORDS
SOURCE Lilium longiflorum (trumpet lily)
ORGANISM Lilium longiflorum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Lilium.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Tzeng, T.-Y. and Yang, C.-H.
TITLE A MADS box gene from Lilium (Lilium longiflorum) is sufficient to
generate dominant negative mutation by interacting with PISTILLATA
(PI) in Arabidopsis thaliana
JOURNAL Plant Cell Physiol. 42 (10), 1156-1168 (2001)
MEDLINE 21573632
PUBMED 11673632
2 (bases 1 to 1039)
REFERENCE Tzeng, T.-Y. and Yang, C.-H.
AUTHORS Direct Submission
JOURNAL Submitted (18-APR-2002) Institute of Biotechnology, National Chung
Hsing University, 250 Kuo-Kung Rd., Taichung, Taiwan 40227, ROC
Location/Qualifiers
source 1. .1039
/organism="Lilium longiflorum"
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/gene="MADS1"
16. .702
/gene="MADS1"
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/codon_start=1
/product="MADS box protein"
/protein_id="AA027456.1"
/db_xref="GI:20531753"
72 AGAGATGGGAGGGGGAAGATAGAGATAAAAAGATAGAGATCCGACGAAACAGCAAGT 131
12 AGCATGCGGGCGGGGAAAGATCGAGATTAAAGATCGAAGACTCGAAGATGCGAGGT 71
QY 132 TACATATTCTTAAGAGAGAGATTGGGATCTGGAAGAGCCAGAGACTCACTGTTCTG 191

ORIGIN

Query Match 32.6%; Score 299.4; DB 8; Length 1039;
Best Local Similarity 67.6%; Pred. No. 1.5e-58;
Matches 471; Conservative 0; Mismatches 211; Indels 15; Gaps 3;

Db 72 CACTTACTGGAAGCCCGGACCGGAATCATCAAGAAAGCAGCTGAGCTCATGTGCTCTG 131

QY 192 TGAATGCTCAGGTCTCTCTCATCATGTTTCTGACACAGAAATGGCTGATTAATGCGAG 251

Db 132 TGAATGCGAAGTCTCTCTCTTATGTTCTTCACAGACCGGGAAGCTGTCAAGATTCGACG 191

QY 252 CCCCTCTACTGATATTAAAGGGATATTATGAGAGTACCAAGTTGTGATCTGGAATGATCT 311

Db 192 CCCCTCCACAGACACGAAAGATCTTCGACCGCTACACAGCTGTCTGGGATCAACCT 251

QY 312 ATGAATGCTCAGTATGAGAGATGAGAAATGCGCTGAGCATCTGAATGATTAACCA 371

Db 252 CTGAGAGGCGCAATACGAAATGCAAAACCTTTGACCACTTGAGCGAGATCAATCG 311

QY 372 AAACCTGAGAGAGAGATTAGAGAGAAAGGGGAGAAATGGAGGCGATGACATTA 431

Db 312 CAACCTTCGACAGAGATGACCGCAGAGATGGGGGAGAGCTGATGATTTGACATCA 371

QY 432 GCAACTGCGCGGTCTTATGAGCAAACTTTGAAAGTCTCTTGAATTTGTTAGGCTATGAA 491

Db 372 GGAAGCTGCGCGGTCTTATGAGCAAAATTTGACGAAAGCTCAAGCTCGTTGCTACCGCAA 431

QY 492 GTATCATGTATGCGCACACAACTGACCTTACAGAAAGCTTAAGCAAGCA 551

Db 432 GTATCATGTATTAACACTGACAGAGACTTACAGAAAGGTCAAAACCTCGAAG 491

QY 552 AACTTACCGGCTCTTAATACATGAATG-----GATATGAAGAGAGAAATCCGAA 602

Db 492 AGCACAAGAACTTGTCTCGGTGACCTGTGAATCGAGAGATGAAAGATGAGATCCAGT 551

QY 603 CTACGCTTTTATATGAGAAACCAAGATGATTTATGAAATTCATTTCCATGTGTGA 662

Db 552 CTATGCTT---ATGTGACGAAAGACCCAGCAATATGATGCGGCTGTGCTGCGCAA 608

QY 663 TGAATGCTCAGATGTTTCTTATAGGTTGTTCAATCCGAAATGAGCCAACTGCTTG 722

Db 609 TGGGCTTCTCATCTGATGAGATTCG---AGTCCAAAGGAGCCAGCCAACTGCAATG 665

QY 723 TTTAGTTATGATCAGATGATCTTATGCTTGAATTA 759

Db 666 GATGGTTATGCTCCCATGATCTCCGATGCTGCTTG 702

RESULT 9 AF209729 833 bp mRNA linear PLAN 01-DEC-2000

LOCUS AF209729

DEFINITION Hemerocallis hybrid cultivar putative MADS box transcription factor (MADS1) mRNA, complete cds.

ACCESSION AF209729

VERSION AF209729.1 GI:11494136

KEYWORDS

SOURCE ORGANISM Hemerocallis hybrid cultivar (daylily)

REFERENCE 1. Hemerocallis hybrid cultivar Eukaryotic Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Hemerocallidaceae; Hemerocallis.

REFERENCE 2. (bases 1 to 833) Molecular changes during the expansion and senescence of ethylene-insensitive daylily flowers Thesis (1999) University of California, Davis

REFERENCE 3. (bases 1 to 833) Lange, N.E., Valpuesca, V., Napoli, C.A., Labavitch, J.M. and Reid, M.S. Direct Submission Submitted (30-NOV-1999) Environmental Horticulture, University of California, Davis, CA 95616-8587, USA

FEATURES

source 1..833

1. Organism="Hemerocallis hybrid cultivar"

2. mol_type="mRNA"

3. /cultivar="Cradle Song"

4. /db_xref="taxon:29711"

5. /tissue_type="petals"

gene 1..833

CDS /gene="MADS1"

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Query Match 32.2%; Score 295.6; DB 8; Length 833;

Best Local Similarity 66.9%; Pred. No. 1,2e-57;

Matches 459; Conservative 0; Mismatches 209; Indels 18; Gaps 2;

196 GCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAATGGCTGATTAATCTGACGCCC 255

Db 121 GCTGACCTGTCAATCATCATGTTCTGAGACCGGGAAAGTTCCGATTTGACGCCCC 180

QY 256 TCTATGATATTAAAGGATATATGAGAGTACCAAGCTTGTGATGGAATGATCTATG 315

Db 181 GGCATGACACGAAAGCGGTGTTGAGAGATATCAGAGCGACGACGAAACTTGTG 240

QY 316 AATGCTCAGTATGAGAGATGAGATACCTGAGCATCTGATGATTAACCAAA 375

Db 241 AGTACACATATGAGAAATGCAAAACACTTGAATATCTCAGAGATCAACATAT 300

QY 376 CTGAGAGAGAGATTAGAGAGAGAGAGAGAAATGGAGGATGACATTAAGCAA 435

Db 301 TTGGCAGAGAAATTAAGCAGAGAGATTGAGAGAACTTATGATGATGATTTCAAGAA 360

QY 436 CTGCGGCTTTCAGCAAACTTTGAAAGTCTTTGAATTTGATGATGAAATGAT 495

Db 361 CTGCGGCTTTCAGCAAACTTTGAAAGTCTTTGAATTTGATGATGAAATGAT 420

QY 496 CATGTGATTCGCAACAACTGACCTTACAGAAAGCTTAAGCAAGGAAACT 555

Db 421 CATGTGATTAACCACTGACTGATACCTACAGAAAGGTAAGAAATTCAGAAAGCA 480

QY 556 TACCGGCTCTAATACATGAACTGATATGAAAGAGAGATCCGAATCGGTTTAT 615

Db 481 CACAAGACTTTGCTGACAGAACTTGAAGAGCACTGTA-----TGATAT 525

QY 616 GTAGAAAACAGATAGATTTATGAATTCGATTCGATGATGATGATGATGATG 675

Db 526 GCGATGAGAGACCAAGCACTATGATGATGATGATGATGATGATGATGATGATG 585

QY 676 ATGTTTCTTATGAGGTTGTTCAATGAGGCAATGCTGTTGATGATGATGATG 735

Db 586 ATGATGCTTACCG---AGTTCACCAAGCCAGCAAACTTCATGAGATGATGATG 642

QY 736 TCACATGATCTTACCTTGCATTAATG 761

Db 643 CCAATGATCTTCTGCTTGCATGATG 668

RESULT 10 AF230706 938 bp mRNA linear PLAN 02-JUN-2000

LOCUS AF230706

DEFINITION Tacca chantieri MADS box transcription factor AP3 mRNA, partial

ACCESSION AP230706 cds.
 VERSION AP230706.1 GI:8163953
 KEYWORDS Tacca chantleri
 SOURCE Tacca chantleri
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales;
 Dioscoreaceae; Tacca.
 REFERENCE 1 (bases 1 to 938)
 AUTHORS Kramer, E.M. and Irish, V.F.
 TITLE Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
 JOURNAL Int. J. Plant Sci. (2000) In press
 REFERENCE 2 (bases 1 to 938)
 AUTHORS Kramer, E.M. and Irish, V.F.
 TITLE Direct Submission
 JOURNAL Submitted (03-FEB-2000) MCB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA
 FEATURES
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 1. .938
 /organism="Tacca chantleri"
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 /translation="MGIMKKAKELTVLQDAEVLIMSSNGKFAEYCSPTDPRKYVD
 RYQVYGDIDMSQYERMONNLHLEIRNRLREIRQRGDELDELKELGLN
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 ORIGIN
 Query Match 31.9%; Score 292.8; DB 8; Length 938;
 Best Local Similarity 67.9%; Pred. No. 5,1e-57;
 Matches 440; Conservative 0; Mismatches 202; Indels 6; Gaps 2;
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 4 GGGATCATGAAGAAGCCAGAGCTCAGTCTCTGTGATGCTCAGTCTCTCTATC 63
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 214 ATGTTCTCAAGCAGAGAAAGTTGGCTGATTAATGCAAGCCCTCTACTGATTAAGGG 273
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 64 ATGTTCTCAAGCAGTGGCAAGTTCCGAGTACTGAGTCTCTCAAGCAGTACGAGAG 123
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 274 ATATATGAGAGGTACCAAGTGTGATGCAATGATGATGATGATGATGATGATGATG 333
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 124 GTTTACATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATG 183
 |||||
 334 ATGCAAGATACGCTGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 393
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 184 ATGCAAAATTAACCTGATCATCTGAGAGATCAACGGAATCTTCAAGAGAAATTAAG 243
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 394 AGAGAGAGAGAGAGATGAGAGGATGAGATCAAGCACTGCGCGCTTTGAGCAA 453
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 244 CAAAGAGCGGCGGAGATCTTGAAGGCTTGAATCAAGAACTGCGTGTCTTGAAGCAA 303
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 454 ACTTTGGAAGAGTCTCTTAAGATGTTAGGATGAGATGAGATGAGATGAGATGAGATGAG 513
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 304 AATGTGATGAGGCTTTGAGGATTTGCTGTAAGAAATATCAATGTTATCAACCAACAG 363
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 514 ACTGACACTTACAGAAAGAGCTTAAAGCAAGAGAACTTACCGGCTTATATCAT 573
 |||||
 364 ACCGATCATATTAAGAGAGCTGAAGATTTCCATGAAGTCAAGAACTTATATCGA 423
 |||||
 574 GAACTGATATGAAGAGAGATCCGAACTACGTTTAAATGTAAGAAAACAGAGTGA 633
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 424 GAACTGAGATGAGAGATGAGACCCAGTTACGGGTT---CGCGCAATGATGATCTACT 480
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Query 634 ATTATGAATAATTCATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 693
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 Db 481 AACTAGACAGCGCTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 537
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 Query 694 GTTCATCCGAAATCAGCCCAATCTGCTGTTGTTAGATTGAATCAATGATCTTACGCTT 753
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 Db 538 GTTCACCCAGCAGCAGCAATCTCCATGAAATGATGATGATGATGATGATGATGATGATG 597
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 Query 754 GCATATGACAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 801
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 Db 598 GCATGAACATGCGTGAAGCTGCTTCTTGAATGCTGATGATGATGATGATGATGATG 645
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 RESULT 11
 LOCUS AY337750 651 bp mRNA linear PIN 31-JUL-2004
 DEFINITION Eupomatia bennettii APTALMA3-like protein AP3-1 mRNA, complete cds.
 ACCESSION AY337750
 VERSION AY337750.1 GI:37993050
 KEYWORDS
 SOURCE Eupomatia bennettii
 ORGANISM Eupomatia bennettii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; magnolids; Magnoliales;
 Eupomatiaceae; Eupomatia.
 REFERENCE 1 (bases 1 to 651)
 AUTHORS Kim, S., Solter, D.E. and Solter, P.S.
 TITLE pre-angiosperm duplication of floral genes and regulatory tinkering at the base of flowering plants
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 651)
 AUTHORS Kim, S., Solter, D.E. and Solter, P.S.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUL-2003) Dept. of Botany, University of Florida, P.O. Box 118526, Gainesville, FL 32611, USA
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 ORIGIN
 Query Match 31.1%; Score 285.4; DB 8; Length 651;
 Best Local Similarity 68.4%; Pred. No. 2.6e-55;
 Matches 410; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
 CDS
 76 ATGGGAGGGGGAAGATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 135
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 Db 1 ATGGGAGGAGAAAGATCGAGTAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 60
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 Query 136 TATTTAAGAGAGAGTGGATTAAGTAAAGAGCCAGAGAGTCACTGTTCTGTGAT 195
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 Db 61 TATTCAGAGGAGAGAGTGGATTAAGTAAAGAGCTTAAGAGAGTCACTGTTCTGTGAT 120
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 Query 196 GCTCAGTCTCTCTCATCATGTTCTCAAGCAGAGAAATTTGGCTGATTAAGTCAAGCCCC 255
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 Db 121 GCTGAGGTTCTCTTTATGTTCTCAATACGGAAGTTCTCGAAATACGTACCCCT 180
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 Query 256 TCTACTGATTAAGGAGATATATGAGAGTACAGAGTGTGATGATGATGATGATGATGATG 315
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 Db 181 TCTACACGACTAAGAGATTTTCGATCGTTACAGAGAGTTTCAAGCAACCACTGTGG 240
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 Query 316 AATGCTCAGTATGAGAGATGAGATTAAGTCAAGAGATGATGATGATGATGATGATGATG 375
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Db 241 AATTCTATTACGAGAAATGCAAGCTCACTTGAAACAACTCAAGAGATTAATACAT 300
 QY 376 CTGAGGAGAGATTTAGAGAGAGAGAGAGAGATTTGAGCGCATGACATTAAGCAA 435
 Db 301 CTCGGAGGAGATCAGCAAGAGATTGGTAGAGATCTGAGAAATCTAGAAATGAGAG 360
 QY 436 CTGCGCGCTCTTGAGCAACTTTTGAGAGAGTCTTTGAAATTTGTAGCATAGAAATAT 455
 Db 361 CTGCGCGCTCTTGAGCAAAATCTGAGAGATTTCTAAATTTGTTCTGAGAGAAATAT 420
 QY 496 CATGTATGCGCACAACTGACCTTACAGAAAAAGCTTAAGACACAGGAAACT 555
 Db 421 CATGTATGCGCATCTCAAACTGAGACTTCAAGAAAAAGCTGAGAACTTGACAGAA 480
 QY 556 TACCGCGCTCTAATACATGAACTGATATGAGAGAGATTCGAACTACGTTTAAAT 615
 Db 481 CATGACAGTTTAGTACGTCATTTGAGAGACAGCTGAGATGGGATATGGTT---G 537
 QY 616 GTAGAAAACAGAGATGATTTATGAAATTCGATTCGATGATGATGATGATGATGAT 674
 Db 538 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596

RESULT 12

LOCUS AY337751 651 bp mRNA linear PLN 31-JUL-2004
 DEFINITION Eupomatia bennettii APETALA3-like protein AP3-2 mRNA, complete cds.
 ACCESSION AY337751
 VERSION AY337751.1 GI:37993052
 KEYWORDS
 SOURCE Eupomatia bennettii
 ORGANISM Eupomatia bennettii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; magnoliids; Magnoliales;
 Eupomatiaceae; Eupomatia.

REFERENCE 1 (bases 1 to 651)
 Kim, S., Soltis, D.E. and Soltis, P.S.
 Pre-angiosperm duplication of floral genes and regulatory tinkering
 at the base of flowering plants
 Unpublished
 JOURNAL 2 (bases 1 to 651)
 Kim, S., Soltis, D.E. and Soltis, P.S.
 Direct Submission
 Submitted (09-JUL-2003) Dept. of Botany, University of Florida,
 P.O. Box 118526, Gainesville, FL 32611, USA
 FEATURES
 SOURCE location/Qualifiers
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Query Match 31.1%; Score 285.4; DB 8; Length 651;
 Best Local Similarity 68.4%; Pred. No. 2.6e-55;
 Matches 410; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 76 ATGGGAGGGGGAATAGATTAATAAAGATAGGAATCCGAGAAAGAGCAAGTTACA 135
 Db 1 ATGGGAGAGGAAAGATCAGATTAATAAAGATAGGAATCCGAGAAAGAGCAAGTACT 60
 QY 136 TATTCTAAGAGAGAGTTGGATCTAGAAAGAGGCAAGAGCTCATGTTCTCTGTGAT 195
 Db 61 TACTGGAAGAGAGGATGGATTTATGAAGAAAGCTTAAGAGACTTCTCTCTCGCAT 120

QY 196 GCTCAGGTCTCTCATCATGTTCTCAGACAGAAAGTGGCTGATTACTGACCCC 255
 Db 121 GCTAGGTTCTCTTAATATGTTCTCAATACCTGGCAAGTTCTCGAATACCTAGCCCT 180
 QY 256 TCTACTGATTTTAAGGGGATATATGAGAGTACAGGTTGTGACTGAAATGATCTATGG 315
 Db 181 TCTACAGAGCTAAGAAAGATTTTCATGCTTACCAAGATTTCAAGACCAACTTGTTGG 240
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 Db 361 CTGCGCGCTTTGAGCAAAATCTGAGAGATTTCTATCAAAATTTGTTGTGAGAGAAAGTAT 420
 QY 496 CATGTATGCGCACACAACTGACACTTACAGAAAAAGCTTAAGACACAGGAAACT 555
 Db 421 CATGTATGCGCATCTCAAACTGAGACTTACAGAAAAAGCTGAGAAACTTGACAGCA 480
 QY 556 TACCGCGCTCTAATACATGAACTGATATGAGAGAGAAATCGAACTACGTTTAAAT 615
 Db 481 CATGACAGTTTAGTACGTCATTTGAGAGACAGAGCTGAGATGGGATATGGTT---G 537
 QY 616 GTAGAAAACAGAGATGATTTATGAAATTCGATTCGATGATGATGATGATGATGATGAT 674
 Db 538 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596

RESULT 13

LOCUS AB050649 852 bp mRNA linear PLN 31-OCT-2001
 DEFINITION Magnolia praecocissima mRNA for putative MADS-domain transcription
 factor MpMADS7, complete cds.
 ACCESSION AB050649
 VERSION AB050649.1 GI:16549069
 KEYWORDS
 SOURCE Magnolia praecocissima
 ORGANISM Magnolia praecocissima
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; magnoliids; Magnoliales;
 Magnoliaceae; Magnolia.

REFERENCE 1
 Ito, M., Shibata, S., Tanabe, Y. and Hasebe, M.
 Organ identities in Magnolian flower
 Unpublished
 JOURNAL 2 (bases 1 to 852)
 Ito, M., Shibata, S. and Hasebe, M.
 Direct Submission
 Submitted (31-OCT-2000) Motomi Ito, University of Tokyo, Department
 of Systems Sciences, Graduate School of Arts and Sciences; 3-8-1
 Komaba, Meguro-ku, Tokyo 153-8902, Japan
 E-mail: cmico@mail.ecc.u-tokyo.ac.jp, Tel: 81-3-5454-6638,
 Fax: 81-3-5454-6638
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Query Match 31.1%; Score 284.8; DB 8; Length 852;
 Best Local Similarity 70.7%; Pred. No. 3.ee-55;
 Matches 379; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

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QY 76 ATGGAGAGGGGGAAGATAGAGATAAAAAGATAGAGATCCGACGAACAGCAAGTTACA 135
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QY 196 GCTCAGAGTCTCTCATCATGTTCTCAAGACAGGAAGTTGGCTGATTACTGCAAGCC 255
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QY 256 TCTACTGATATTAAAGGGATATATGAGAGGTACAGGTTGTGACTGGAATGATCTATG 315
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QY 376 CTGAGAGAGGAGATTGAGAGAGAGGAGGAGAAATTGAGGCAATGACATTAAGCAA 435
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QY 436 CTGCGGGTCTTGAAGCACTTTGGAAGAGTCTTTGAATGTTAGGCATAGAAATAT 495
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QY 556 TACCGGCTCTATPACATGAACTGATATGAAAGAGAGAAATCGAAGCTACGGGTT 611
 DB 481 CACGCAAAATTAATTGCTCATTTGAGAGGTCAGAGCTGAGAACGGGCTTACGGCTT 536

RESULT 14 830 bp mRNA linear PLN 21-AUG-2004
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 LOCUS Alpina hainanensis AP3-like MADS-box protein (MADS) mRNA, partial
 DEFINITION cdb.

ACCESSION AY621154 GI:51243293
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Alpina hainanensis
 Alpina hainanensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
 Zingiberaceae; Alpina.

REFERENCE
 AUTHORS Song,J.J., Ma,W., Liao,J.P. and Tang,Y.J.
 TITLE Characterization of class B and C floral organ gene from Alpina
 1 (bases 1 to 830)

JOURNAL
 REFERENCE 2 (bases 1 to 830)
 AUTHORS Song,J.J., Ma,W., Tang,Y.J., Liao,J.P. and Luo,D.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAY-2004) South China Botanical Garden, Chinese
 Academy of Sciences, Guangzhou, Guangdong 510650, China

FEATURES
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CDS

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 KRSDYCSPTNTKST FDRYOVSGLINSAOYEROMNNLRKEINRLREIRBOMG
 ELDGMDIKELRGLEONDEALKVTRANKRYHTISGTETRYKKVYSQEAHONLHQL
 EKMDHGYMTVDVDPFAHPMYSIKVQPNPDALRISVASHHDLRLA"

ORIGIN

Query Match 30.8%; Score 282.6; DB 8; Length 830;
 Best Local Similarity 73.0%; Pred. No. 1.2e-54;
 Matches 363; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 101 AAAAGATAGAGATCCGACGAACAGCAAGTTACATATTCTAAGAGAGAGTTGGATAC 160
 DB 2 AGAAGATAGAGAACCAACCAACAGCAGAGTGAATTATTCAGAGAGAGTGAAGATCA 61

QY 161 TGAAGAGCCCAAGAGCTCATGTTCTCTGTGATGCTCAGGTTCTCTCATCATGTTCT 220
 DB 62 TGAAGAGCCCAAGAGCTCATGTTCTCTGTGATGCTCAGGTTCTCTCATCATGTTCT 121

QY 221 CAAACACAGAAAGTTGGCTGATTAAGTCTGAGAGCCCTCTACTGATATTAAAGGAAATATG 280
 DB 122 CCAAGCAGGCGAAGTTCTGTGATTAAGTCTGAGAGCCCTCTACTGATATTAAAGTAT 181

QY 281 AGAGTACCAAGTGTGACTGGAATGATCTATGGAATGCTCAGTATGAGAGATGACAG 340
 DB 182 ATGTTATCAACAAAGTGTGAGGATCACTTGAGAGTCAAGTATGAGAAATGCAAA 241

QY 341 ATACGCTGAAGCATCTGATGATTAACCAAACTGAGAGAGAGATTAAGAGAGAGA 400
 DB 242 ATATATGAAACGCTTCAAGAGATCAACCGTAACTCCGAGAGAAATTAAGCAAGGA 301

QY 401 AGGGAGAGAAATTGAGGGCATGACATTAAGCAACTGCGGGTCTTGAGCAAACTTTGG 460
 DB 302 TGGGTAAAGTCTCGATGAGATGACATTAAGAACTGGCGGTCTTGAGCAAACTTTGG 361

QY 461 AAGATCTCTTAAGATTGTTAGCATGAGAAAGTATCATGTATCGCACACAACTGACA 520
 DB 362 ATGAGGCATTTAAAGTTGTTGCAATGAGAAATATCATGTATGACACTCAACACAGAGA 421

QY 521 CTTAACAAGAAAGCTTAAGCAACAAGGAAACTTACCGCGCTCTTAATCATGAACTGG 580
 DB 422 CCTTACAAGAAAGGTAAGAGCTCCCAAGAAAGCTTCAAGAAATTTACTGCATCAATTGG 481

QY 581 ATATGAAGAGAGAAAT 597
 DB 482 AGATGAAGATGAACAT 498

RESULT 15 1002 bp mRNA linear PLN 31-OCT-2003
 AB094965
 LOCUS Tulipa gesneriana TGBEFA mRNA for MADS-box transcription factor,
 DEFINITION complete cdb.

ACCESSION AB094965
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Tulipa gesneriana
 Tulipa gesneriana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;

FEATURES
 source 1..1002


```

REFERENCE
AUTHORS      1
TITLE        Kanno,A., Saeki,H., Kameya,T., Saedler,H. and Theissen,G.
              heterotopic expression of class B floral homeotic genes supports a
              modified ABC model for tulip (Tulipa gesneriana)
JOURNAL      Plant Mol. Biol. 52 (4), 831-841 (2003)
MEDLINE      12856392
PUBMED       13677470
REFERENCE    2 (bases 1 to 1002)
AUTHORS      Kanno,A.
TITLE        Direct Submission
              Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
              School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
              980-8577, Japan (E-mail:kanno@ige.tohoku.ac.jp, Tel:81-22-217-5725,
              Fax:81-22-217-5725)
FEATURES
source       1..1002
              location/Qualifiers
              /organism="Tulipa gesneriana"
              /mol_type="mRNA"
              /cultivar="White Dream"
              /db_xref="taxon:13306"
              /tissue_type="flower"
              1..1002
              /gene="TGDFPA"
              72..758
              /gene="TGDFPA"
              /codon_start=1
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              /protein_id="BAC75970.1"
              /db_xref="GI:30172221"
              /translation="MGRKTIKIKIENSTKROVYTSKRBSGIMKANELTVLDAEVS
              LMPSSTHKLSEFCSESTNQKQIDRYQMTGIMLSAQYKQNTFNHLSQINRIR
              REIKQWBEIDIGLDFSELRLDQMLEALIVGRKYHVIQTETYYKKKVNSEET
              NKULRLVNIEMQBHQVGYIIDDDNSYEGIALANGSSMYEPRVOPSPVLIHGM
              GYGIHDLRLA"

ORIGIN
Query Match 30.8%; Score 282.2; DB 8; Length 1002;
Best Local Similarity 65.6%; Pred. No. 1.4e-54;
Matches 464; Conservative 0; Mismatches 228; Indels 15; Gaps 3;

QY 76 ATGGGAGGGGGAAGTAGATGATAAAAGATAGAGATCCGACGACAGCAAGTTACA 135
DB 72 ATGGGTCGTGGCAAGATCGAGATCGAAGATCGAAGCTCAACCAACCGTCAGGTCACT 131
QY 136 TATTCTAAGAGAGAGGTGGATATCTGAAGAAGGCCAAGAGCTCACTGTTCTCTGTGAT 195
DB 132 TATTCCAAGCTCCGACGTGGGATCATGAAGAAGGCCAAGACTCACTGTCCTTGGCAT 191
QY 196 GCTCAGGTCTCTCATCATGTTCTCAAGCAAGAGAAAGTTGGCTGATTACTCGACGCC 255
DB 192 GCTGAAGTTTCCTATCATGTTTCAAGCACTCAAGACTCTCCAGTCTCGCAGTGAA 251
QY 256 TCTACTGATTAAGGGGATATATGAGAGGTACCGAGTTTGACTGGAATGATCTATGG 315
DB 252 TCCACCATCGAAGAAAGATCTTCGACCGGTACCGAGATGACTGGGATCAACTTGG 311
QY 316 AATGCTCAGTATGAGAGATCGAAGATCGCTGAAGCATCTGAATGATTAACCAAAAC 375
DB 312 AGCGGCAATACGAGAAATGCAAGATACGTTCAACCATCTGAGCCAGATCAACCGTAA 371
QY 376 CTGAGGAAGAGATTAGAGAGAGAGAGAGAGAGAAATTGAAGGCGATGACATAAGCAA 435
DB 372 CTTCGACAGGAGATTAAGCAAGAGAGAGAGAGAGAGCTGATGCTGGACTTCAGCGAG 431
QY 436 CTGCGCGGCTTTGAGCAAACTTTGGAAGATCTCTAGAATTTGTAAGCATGAAGTAT 495
DB 432 CTGCGCGGCTTTGAGCAAAATTTGAGAGAGGCTTTGAAGATTTGTTGAGGAGAGATAT 491
QY 496 CATGTGATCGCACAACCTGACACTTACAGAAAAAGCTTAAGCAACAAGGAAACT 555
DB 492 CATGTGATTTGATCTGACAGCAAAACCTACAGAAAAAGTGAATAATTCGAGGAAACT 551
QY 556 TACCGCGCTTAATACATGAACCTG-----GATATGAAGAAGAGAAATCCGAATAC 606

```

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DB 552 AATAAGAACTTGCTCGAGACCTGGAGACATAGAGATGAAAGATGACATCAAGCTAC 611
QY 607 GGTATTAATGTAAGAAAACAGATGAGATTAATTAAGAAATTCATTCATATGATGAG 666
DB 612 GGTATTAATGAGATGATGACCCGAAACAG--CTATGAGGAGGCGCTTCTGCGAATGG 668
QY 667 TGTCTCAGATGTTTCTTTAGGGTGTTCATCCGATCAGGCCAATCTGCTTGTTTA 726
DB 669 GGAATTAAGATGATGACAGATTCCG--GATCAACCGAGCCAAACCTCCAGCGGATG 725
QY 727 GGTATGAATCAATGATCTTAGCCTTGATATAGAGCAATATAT 773
DB 726 GGTATGACTCATGATCTTGCGCTTGCTTGAAACTCGAATCTT 772

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Job time : 4378 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 08:32:05; Search time 619 Seconds
(without alignments)
8769.633 Million cell updates/sec

Title: US-10-690-246A-1

Perfect score: 917
Sequence: 1 acgcggagatgtagaggaag.....ttttgtttttttttcg 917

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*

1: Geneseq199808: *
2: Geneseq19908: *
3: Geneseq120006: *
4: Geneseq120011bs: *
5: Geneseq120011bs: *
6: Geneseq12002as: *
7: Geneseq12002bs: *
8: Geneseq12003as: *
9: Geneseq12003bs: *
10: Geneseq12003cs: *
11: Geneseq12003ds: *
12: Geneseq12004as: *
13: Geneseq12004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.2	26.7	637	10	ADK59650 Plant DNA
2	236	25.7	1257	6	ADK42257 Corn AP3
3	236	25.7	1257	13	ADK42257 Corn AP3
4	234.8	25.6	681	12	ADK44530 Plant CDN
5	228	24.9	946	6	AAK85392 Nucleocid
6	228	24.9	946	6	ABK88485 Poplar pr
7	228	24.9	946	9	ACB62518 Poplar ho
8	227.2	24.8	681	4	AAK85393 Nucleocid
9	223.2	24.3	989	3	AAK57943 Poplar fl
10	216.6	23.6	989	3	AAK55879 Eucalyptu
11	215	23.4	644	13	ACN53850 Cotton an
12	214.4	23.4	954	3	AAK51525 Arabidops
13	213.8	23.3	1170	3	AAK51790 Arabidops
14	213.2	23.2	988	12	ADK61550 Transcrip
15	211.6	23.1	959	3	AAK40831 Arabidops
16	209.8	22.9	664	10	ADK56100 Plant DNA
17	209.8	22.9	665	10	ADK59635 Plant DNA
18	207.2	22.6	926	6	AAK42259 Soybean A
19	207.2	22.6	926	13	ADK04282 Soybean A
20	203.4	22.2	630	10	ADK59791 Plant DNA

ALIGNMENTS

RESULT 1	ADK59650	standard; DNA, 637 BP.
ID	ADK59650	standard; DNA, 637 BP.
XX	ADK59650;	
XX	AC	
DT	06-MAY-2004	(first entry)
XX	Plant DNA sequence which confers altered metabolic characteristic #7033.	
XX	altered metabolic characteristic; plant; acid metabolism;	
KW	alcohol metabolism; fatty acid metabolism;	
KW	branched fatty acid metabolism; alkaloid metabolism;	
KW	amino acid metabolism; ester metabolism; glyceride metabolism;	
KW	terpene metabolism; isoprenoid metabolism; alkene metabolism;	
KW	aldehyde metabolism; hydrocarbon metabolism; ketone metabolism;	
KW	quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.	
XX	Unidentified.	
OS	Unidentified.	
XX	WO2003020936-A1.	
XX	13-MAR-2003.	
XX	30-AUG-2002; 2002WO-US027884.	
XX	31-AUG-2001; 2001US-0316471P.	
XX	(DOMC) DOW CHEM CO.	
XX	(DOMC) DOW AGROSCIENCES LLC.	
PA	Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;	
PI	Oxley JVB, Croxley R, Reddy AS, Shukla V, Larrina I, Miller BA;	
DR	WPI, 2003-313091/30.	
XX	Novel genes that confer altered metabolic characteristics in Nicotiana	
PT	benhamiana plants, useful for altering the levels of metabolites e.g.,	
XX	acids, fatty acids, amino acids, carbohydrates, hydrocarbons and steroids.	
PS	Claim 1, SEQ ID NO 7033; 2576pp; English.	

21	202.4	22.1	954	3	AAK40685
22	201.2	21.9	498	12	ADP95468
23	200.8	21.9	882	2	AAK51189
24	194.8	21.2	982	4	AAK00104
25	176	19.2	425	12	ADK03168
26	170	18.5	432	12	ADK03170
27	168	18.3	401	12	ADK03167
28	161	17.6	868	4	AAK00103
29	160.4	17.5	407	12	ADK06448
30	159.2	17.4	366	3	AAK57268
31	155.2	16.9	360	12	ADK03169
32	154.4	16.8	947	3	AAK39436
33	153.8	16.8	914	12	ADK01642
34	153.8	16.8	951	12	ADK01552
35	151.8	16.6	914	13	ADK61340
36	151.2	16.5	896	10	ADK5880
37	149.8	16.3	905	3	AAK57204
38	148.6	16.2	474	12	ADP95656
39	148.2	16.2	639	13	ACN53901
40	146.4	16.0	601	13	ACN58761
41	145.6	15.9	742	10	ADK56091
42	144.2	15.7	632	10	ADK55993
43	143.4	15.6	409	3	AAK56790
44	142.4	15.5	649	13	ACN54118
45	142.4	15.5	909	3	AAK35208

QY 495 TCATGTGATGCCACACAACTGACACTTACAAAGAAAGCTTAAAGCAAGGAAAC 554
 DB 550 CCATGTGATGACGACGACGACTGATACCTTCAAGAAAGAGTAAAGCACTGACAGAGGC 609
 QY 555 TTACCGGCGCTTAATCATGATCGATATGAAAGAGAGATCCGAATACGGTTTAA 614
 DB 610 GTTCAAGAACCTTGACAGAGAGCTAGGATGCGGAGAGACCGGCGTTCCGGTACGTGA 669
 QY 615 TGTAGAAACCAAGATGATGAAATTTATGAAATTCGATTCGAATGATGATGTCCTCA 674
 DB 670 CAACAGCGGCGCGCGGCGTCCGCGGAGCGGCGGCGCGCTGGGCGGCGCGCC 729
 QY 675 GATGTTTCTTTAGGCTTGTATCCGAATCAGCCCAATCTGCTTGGTTAGTTATGA 734
 DB 730 GGACATGTAGCCCTTCCGCGTGTGCTCCAGCCAGCCCACTGACGCGCATGCGCTACGG 789
 QY 735 ATCAGATGATCTTAAAGCTTGCAT 758
 DB 790 CTTCACGACCTCCGCTGGGCTA 813

RESULT 3

ADNR04278 standard; cDNA; 1257 BP.

ADNR04278;

04-NOV-2004 (first entry)

Corn Ap3 homologue encoding cDNA SEQ ID NO:45.

XX flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant;
 XX floral development; plant sterility; plant fertility; flowering time;
 XX plant growth rate; inflorescence architecture; tissue culture morphology;
 XX cell division; Ap3 homologue; gene; ss.

XX Zea mays.

XX Location/Qualifiers

XX Key 131..814

XX CDS /product= "Apetala3 (Ap3) homologue"

XX WO2004067723-A2.

XX 12-AUG-2004.

XX 29-JAN-2004; 2004WO-US002422.

XX 30-JAN-2003; 2003US-00343477.

XX (PION-) PIONEER HI-BRED INT INC.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Danilevskaya O, Hermon P, Bruggemann E, Shidroun D, Ananiev E;

XX Rafalekri JA, Sakai H, Cahoon E, Cahoon R, Klein T;

XX WPI; 2004-580996/56.

XX P-PDB; ADNR04279.

XX New polynucleotides, specifically nucleic acid fragments encoding (Ap3)

XX flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3)

XX homologs, useful for floral development, e.g. engineering plant flowering

XX time.

XX Claim 6; SEQ ID NO 45; 109pp; English.

XX The present invention describes an isolated polynucleotide comprising a

XX first, second, third, fourth or fifth nucleotide sequence, or their

XX complement encoding a polypeptide either having flowering locus T gene

XX (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also

XX described: (1) a vector comprising the polynucleotide; (2) a recombinant

XX DNA construct comprising the polynucleotide; (3) transforming a cell by

CC transforming a cell with the polynucleotide; (4) a cell comprising the

CC recombinant DNA construct; (5) producing a plant comprising transforming

CC a plant cell with the polynucleotide, and regenerating a plant from the

CC transformed plant cell; (6) a plant comprising the recombinant DNA

CC construct; (7) a seed comprising the recombinant DNA construct; (8) an

CC isolated polynucleotide comprising a first nucleotide sequence, where the

CC first nucleotide sequence contains at least 30 nucleotides, and where the

CC first nucleotide sequence is comprised by another polynucleotide, where

CC the other polynucleotide includes the second, third, fourth, fifth or

CC sixth nucleotide sequence; (9) an isolated polypeptide having FT or Ap3

CC homologue activity, as described above; and (10) isolating a polypeptide

CC encoded by the polynucleotide comprising isolating the polypeptide from a

CC cell containing a recombinant DNA construct comprising the polynucleotide

CC operably linked to a regulatory sequence. The polynucleotides are useful

CC for floral development, e.g. engineering plant sterility/fertility,

CC flowering time, plant growth rate, inflorescence architecture, and tissue

CC culture morphology and the rate of cell division to enhance

CC transformation. The present sequence encodes an Ap3 homologue from the

CC present invention.

XX Sequence 1257 BP; 320 A; 353 C; 340 G; 244 T; 0 U; 0 Other;

XX Query Match 25.7%; Score 236; DB 13; Length 1257;

XX Best local Similarity 59.1%; Pred. No. 2.3e-50;

XX Matches 404; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

QY 75 GATGGGAGGGGGAAGATGAGTAAAGATGAGATCCGACCAAGGAGTAC 134

DB 130 GATGGGCGCGGCAAGATCAGATCAAGCGGATCGAAGACGACCAACCGCAGGTAC 189

QY 135 ATATCTAAGAGAGAGATTGGATCTGAAGAGGCGCAAGAGATCTTCTGTGA 194

DB 190 CTACTCAACCGCGGACGAGGATCATGAAAGGCGCGGACTACCGTCTTCGA 249

QY 195 TGCTCAGGTCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGCTGATTACGACCC 254

DB 250 CGCCAGGTCCCATATCATGTTCTCTCACCGGCAAGATACCAAGATTGACGCC 309

QY 255 CTCTAGTATTAAGGAGATATATGAGAGTACAGGTTGTGACTGGATGATGAT 314

DB 310 CGGAACCGACATCAAGACATCTTGTGACCGGTACAGAGCCATCGGACCAAGCTATG 369

QY 315 GAATGCTCAGTATGAGAGATGAGCAATAGCTGAAGCATCTGAATGATGAACAAA 374

DB 370 GATGAGAGATGATGAGATATGAGCGCAGCTGAGCATCTCAAGACATCAATCTGG 429

QY 375 CCTGAGAGAGAGATTGAGAGAGAGAGAGAGATTGAGAGGCAATGACAATAAGCA 434

DB 430 TCTGCGACAGAGATTAGGCAAGAGATGGCGAGAGATCTGACAGTCTGACATTGACGA 489

QY 435 ACTGCGGCTCTTGAAGAACTTTGAGAGAGTCTTTGAAATTTGAGCATAGAAAGTA 494

DB 490 GCTGCGGCGCTCGAGAAACGTCGAGCGGCTCTCAAGAGAGTTCGCAATAGAAAGTA 549

QY 495 TCATGTGATGCCACACAACTGACACTTACAAAGAAAGCTTAAAGCAAGGAAAC 554

DB 550 CCATGTGATGACGACGACGACTGATACCTTCAAGAAAGAGTAAAGCACTGACAGAGGC 609

QY 555 TTACCGGCGCTTAATCATGATCGATATGAAAGAGAGATCCGAATACGGTTTAA 614

DB 610 GTTCAAGAACCTTGACAGAGAGCTAGGATGCGGAGAGACCGGCGTTCCGGTACGTGA 669

QY 615 TGTAGAAACCAAGATGATGAAATTTATGAAATTCGATTCGAATGATGATGTCCTCA 674

DB 670 CAACAGCGGCGCGGCGTCCGCTGGAGCGGCGCGCGCGCTGGGCGGCGCGCC 729

QY 675 GATGTTTCTTTAGGCTTGTATCCGAATCAGCCCAATCTGCTTGGTTAGTTATGA 734

DB 730 GGACATGTAGCCCTTCCGCGTGTGCTCCAGCCAGCCCACTGACGCGCATGCGCTACGG 789

QY 735 ATCAGATGATCTTAAAGCTTGCAT 758

DB 790 CTTCACGACCTCCGCTGGGCTA 813

RESULT 4
ADJ44530
ID ADJ44530 standard; cDNA; 681 BP.
XX
AC ADJ44530;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant cDNA #5530.
XX
XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.
XX
OS Eukaryota.
XX
XX US2004016025-A1.
XX
PD 22-JAN-2004.
XX
PF 26-SEP-2002; 2002US-00260238.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.
XX
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREBS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
XX
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;
XX
DR WPI; 2004-190374/18.
XX
XX
PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
PS Example 13; SEQ ID NO 5530; 230bp; English.
XX
CC The invention relates to plant nucleotide sequences that direct seed-
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 681 BP; 156 A; 213 C; 215 G; 97 T; 0 U; 0 Other;
Query Match 25 6%; Score 234.8; DB 12; Length 681;
Best Local Similarity 65.8%; Pred. No. 3.7e-50;
Matches 341; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
QY 76 ATGGGAGGGGGAAGATAGATATTAAGATAGAGATCCGACGACGAGGAGTTACA 135
DB 1 ATGGGCGCGGCGAAGATCGAGATCAAGCGGATCGAAGACGCCACGACCGGAGTACC 60
QY 136 TATCTTAAGAGAGAGTTGGATTAAGTAAAGAGCCAGAGCTCATCTTTCTGTGTAT 195
DB 61 TACTCCAAAGCGCGGACGCGGATCATGAAGAGGCGCGAGACTACCTGTCTGCGCAC 120
QY 196 GCTCAGAGTCTCTCTCATCTGTTTCAACACAGAGAAAGTTGGCTGATTACTGACGCCCC 255
DB 121 GCCCAGGTGCGCATCATCTGTTCTTCACCGGCAAGTACACGAGTTCTGACGCCCC 180
QY 256 TCTACTGATATTAAAGGGATATATGAGAGGTACAGAGTTGTGACTGAATGATCTATGG 315
DB 181 GGAAACGACATCAAGACATCTTTGACCGGTACAGACGACCATCGGACCGACCTATGG 240
QY 316 AATGCTCAGTATGAGAGATGCAAGATACGCTGAAGCATCTGAATGAGATTACCAAAAC 375
DB 241 ATGAGCAGATATGAGAAATATGACAGCGACGCTGAGCATCTCAAGACATCAATCGTGT 300
QY 376 CTGAGAAAGAAATTGAG 435
DB 301 CTGGGACAGAGATTAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 436 CTGCGCGCTCTTGAGCAAACTTGGAAAGAGCTCTTGAATTTGTTAGGAGTAAAGTAT 495
DB 361 CTGCGCGGCTCTGAGGAAAACGTCAGCGGCTCTCAAGAGGTTGCGCATGGAAGTAC 420
QY 496 CATGTATGCGCACACAACTGACCTTCAAGAAAGAGCTTAAAGCAAGGAGAACT 555
DB 421 CATGTATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 480
QY 556 TACCGCGCTCTAATACATGAACGTGATGAAAGAGA 593
DB 481 TACAAAGACCTGACGAGAGGCTAAGGATGCGGAGAGA 518
RESULT 5
AAF85392
ID AAF85392 standard; cDNA; 946 BP.
XX
XX
AC AAF85392;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of the floral homeotic protein PTD.
XX
XX Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
KM LFY; FLORICULM; FLO; DEFICIENS; DBF; AGAMOUS; AG; transgenic plant;
KM fertility; sterility; ss.
XX
OS Populus balsamifera.
XX
FH Key Location/Qualifiers
FT CDS 1..684
FT /tag= a
FT /product= "PTD"
XX
PN CA2319853-A1.
XX
PD 01-APR-2001.
XX
PP 02-OCT-2000; 2000CA-02319853.
XX
PR 01-OCT-1999; 99US-00410464.
XX

Db 421 CATGTATCAAAACAAAACGAACTACAGAGAGAGTGAAGATTGAGAGAGA 480
 Qy 556 TACCGCGCTCTTAATACATGAATGATATGAAAAGAGAAATCCGAATCAGGTTTAAAT 615
 Db 481 CATGGAACCTCTTGATGAAATGAAAGCAAACTAGAGATGACAGTATGGTTAGTG 540
 Qy 616 GTAGAAAACCAAGTGAATTTATGAAATTCGATTCCATGGTGAATGAGTCTCCAG 675
 Db 541 GACAAATGAAGCTGCTGTGGCACTTGCATAATGGGGCTTCCAACTCTATGCAATCCGCTG 600
 Qy 676 ATGTTTTCCTTGAAGGTTGTTCAATCCGATCAGCCCAATCGTGTGTTAGGTTATGAA 735
 Db 601 CATCAGCGGCAACAACCAACCACTATCTTCACTTGAAGATGATTTGA 660
 Qy 736 TCACATGATCTTAGCCCTTGATTA 759
 Db 661 GCCCATGAACTTGCCCTTCTTGA 684
 RESULT 8
 ID AAF85393 standard; cDNA; 681 BP.
 AC AAF85393;
 DT 23-JUL-2001 (first entry)
 DE Nucleotide sequence of the floral homeotic protein PTD.
 KM Floral homeotic gene; PTD, PTLF, PTAG-1, PTAG-2; floral tissue; LEAFY;
 KW LFY; FLO/ICADLA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 fertility; sterility; ss.
 OS Populus balsamifera.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..681
 FT /*tag= a
 FT /product= "PTD"
 PN CA2319853-A1.
 XX
 PD 01-APR-2001.
 XX
 PF 02-OCT-2000; 2000CA-02319853.
 XX
 PR 01-OCT-1999; 99US-00410464.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Rottman WH, Strause SH, Brunner AM, Sheppard LA,
 XX
 DR WPI; 2001-336098/36.
 DR P-PSDB; AAB86435.
 XX
 PT Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility.
 XX
 PS Claim 25; Page 42-43; 69pp; English.
 XX
 CC The present sequence encodes a floral homeotic protein, designated PTD.
 CC It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PTLF, PTAG-1 and PTAG-2 proteins. The floral
 CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 CC LEAFY (LFY) and FLO/ICADLA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamens
 CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility

XX
 SQ Sequence 681 BP; 228 A; 148 C; 157 G; 148 T; 0 U; 0 Other;
 Query Match 24.8%; Score 227.2; DB 4; Length 681;
 Best Local Similarity 58.4%; Pred. No. 3.3e-48;
 Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;
 Qy 76 ATGGGGAGGGGGGAGATAGAGATPAAAGATGAGAAATCCGACGAAGCAAGGTTTACA 135
 Db 1 ATGGGTCGTGAGAAAGATGAAATCAAGAAATGGAAGATGAAAGCCCAACAGCAAGTCACC 60
 Qy 136 TATTTAAGAGAGAGAGTGGATGATCTGAAAGAGCCAGAGCTCATCTGTTCTGTGAT 195
 Db 61 TATCGAAGAGAGAAATGATATTTTCAAGAAAGCCCAAGAACTCATCTGATTTGAT 120
 Qy 196 GCTCAGGTCCTCTCATCATGTTTCTCAAGCAGAGAAAGTTGGCTGATTAATCAAGCCCC 255
 Db 121 GCTAAGGTCCTCTTATCATGTTTCTCCAACTACAACTCAATGAGTACATTAAGCCCC 180
 Qy 256 TCTACTGATATTTAAGGGGATATATGAGAGGTACAGGTTGTACTGGAATGATCTATGG 315
 Db 181 TCACATCGCAAGAAAGATCTAGATCAATATCAAGACCTTTAGCATAGATCTGTGG 240
 Qy 316 AATGCTCAGTATGAGAGATGACAGAAATACGCTGAGCATCTGATGATTAACCAAAAC 375
 Db 241 GGCATCTCAATACAGAAATATGCAAGACACTTGAAGAGCTGATATCAATCATTAAG 300
 Qy 376 CTGAGAGAGAGATTGAGAGAGAGAGGAGAGAAATTGAGGCAATGACATTAAGCAA 435
 Db 301 CTGAGACAAAGAAATCAAGGCAGAGAGAGAGAGGCGCTGAATATCTGACATTAATGAT 360
 Qy 436 CTGCGGCTCTTGAAGCAATTTGAAAGACTCTCTTAAGATTGTTGGCATAGAAAGTAT 495
 Db 361 CTGCGGCTCTTGAAGCAATATGACTGAAGCCCTTGATGCTGTGCTGCAAGAGATAC 420
 Qy 496 CATGTATCGCCACACAACTGACACTTACAAAGAAAGCTTAAGCAACAGGAAACT 555
 Db 421 CATGTATCAAAACAAAACGAAACCTTACAGAGAAAGTGAAGATTTAGAGAGAGA 480
 Qy 556 TACCGCGCTCTTAATACATGAATCGATATGAAAAGAGAAATCCGAATCAGGTTTAAAT 615
 Db 481 CATGGAACCTCTTGATGAAATGAAAGCAAACTAGAGATGACAGTATGGTTAGTG 540
 Qy 616 GTAGAAAACCAAGTGAATTTATGAAATTCGATTCCATGGTGAATGAGTCTCCAG 675
 Db 541 GACAAATGAAGCTGCTGTGGCACTTGCATAATGGGGCTTCCAACTCTATGCAATCCGCTG 600
 Qy 676 ATGTTTTCCTTGAAGGTTGTTCAATCCGATCAGCCCAATCGTGTGTTAGGTTATGAA 735
 Db 601 CATCAGCGGCAACAACCAACCACTATCTTCACTTGAAGATGATTTGA 660
 Qy 736 TCACATGATCTTAGCCCTTGC 755
 Db 661 GCCCATGAACTTGCCCTTCC 680
 RESULT 9
 ID AA257943 standard; cDNA; 924 BP.
 AC AA257943;
 DT 11-APR-2000 (first entry)
 DE Poplar floral homeotic gene PTD cDNA.
 DE Poplar floral homeotic gene PTD cDNA.
 KM Poplar; PTD; floral homeotic gene; transgenic plant; sterility;
 KW fertility; ss.
 OS Populus balsamifera subsp. trichocarpa.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..684

/*tag= a
/note= "the coding region is also specifically claimed in
Claim 1"

CA2227940-A1.
06-OCT-1999.
07-APR-1998; 98CA-02227940.
06-APR-1998; 98US-00080851.
(UYOR-) UNIV OREGON HEALTH SCI.
Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
WPI; 2000-106662/10.
P-PSDB; AAY58654.

Nucleic acid from *Populus trichocarpa* genes, useful for producing transgenic plants, particularly trees, with modified fertility characteristics such as sterility.

Claim 1; Page 46-47; 92pp; English.

The present sequence is that of cDNA encoding *Populus balsamifera* subsp. *trichocarpa* PTD protein (see AAY58654). The PTD gene (see AAZ57942) is 1 of 4 newly identified floral homeotic genes from this poplar species. It is a homologue of *DEFICIENTS* and is expressed strongly in stamen primordia from the onset of organogenesis, and is also expressed at low levels in carpel primordia. The invention provides nucleic acid sequences of these 4 *Populus* genes, the corresponding cDNA sequences (see AAZ57942-49) and deduced amino acid sequences (see AAY58454-57). It also provides methods of using the gene and cDNA sequences to produce genetically engineered *Populus* species and other trees having modified fertility characteristics, including sterility. Genetic constructs useful in producing genetically engineered *Populus* and other trees include antisense versions of PTD, dominant negative mutants, and constructs useful for sense suppression. Promoter sequences may be used to obtain floral specific expression of genes such as cytochrome oxidase that may be used in genetic ablation strategies to produce trees having modified fertility characteristics, including sterility. Sterile trees allow increased wood yield and a reduction in the production of allergens such as pollen

Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

Query Match 24.3%; Score 223.2; DB 3; Length 924;
Best Local Similarity 57.9%; Pred. NO. 4e-47;
Matches 396; Conservative 0; Mismatches 288; Indels 0; Gaps 0;

76 ATGGGAGGGGGAATGAGATTAATAAATAGATAGAAATCCGACGAGCAAGTTACA 135
1 ATGGGTGTGGAAGATTGAATCAAGAAATCCCAAAACAGCAAGCAAGTACC 60
136 TATCTAAGAGAGAGTTGGATCTAGTAAGAGCCCAAGAGACTCACTGTTCTGTGAT 195
61 TACTCGAAGAGAAATGATGATTTTCAAGAAACCCCAAGAACTCATCTGATTTGAT 120
196 GCTCAGGTTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGCTGATTAAGTCAAGCCC 255
121 GCTAAGGTCTCTTATCATATGTTCCCAACATTAACAAACTCATGAGTACATTAAGCCC 180
256 TCTACTGATATTAAAGGAGATTATGAGAGATCCAGAGTTGATCGAATGAGATCTATGG 315
181 TCCACATCGACAAAGAAATCTAGATCAATATAGAAACGTTTAAAGCATAGATCTGTGG 240
316 AATGCTGATATGAGAGATGACAGATTAACGCTGAAGCATCTGATGATTAACCAAAAC 375
241 GGCCTCTAATACGAGAAATATCAAGAGCACTTGAGAGAGTGAATGATCAATCAATAG 300
376 CTGAGAGAGAGATTAAGAGAGAGAGAGAGAGAAATTTGAGAGGCTATGACATTAAGCAA 435
301 CTGAGACAGAAATATCAGGACAGAGAGAGAGAGAGGCGCTGATGATCTGAGCATTTGATCAT 360

436 CTGCGCGGCTTGTAGCAACTTTGGAAGAGTCTTTAGATTGTTAGGCATAGAAAGTAT 495
361 CTGCGCGGCTTGTAGCAACTTTGGAAGAGTCTTTAGATTGTTAGGCATAGAAAGTAT 420
496 CATGTGATGCGCAACACAACTGACATTTAGAGAAAGTTTAAAGCAAGGAAACT 555
421 CATGTGATCAAAACACAAAGTCTTCAAGAGAGAGTGAATTTAGAGGAGAA 480
556 TACCGGCTCTTAATCATGACATGATAGAAAGAGAGAAATCCGAACTAGCGTTTAAAT 615
481 CATGAAACCTCTTGTAGAAATATGAGCAAACTAGAGAGATGACAGATATGTTAGAG 540
616 GTAGAAACCAAGAGTGAATTTATGAAATTTGATTCGAATGATGATGCTCTCAG 675
541 GACAAAGAAAGCTGCTTGTGACATGCAATATGAGGCTTCCAACTCATCATTCGCGCTG 600
676 ATGTTTCTTTAGAGGTTGTCATCCGAATCAAGCCCAATCTGCTTTAGGTTATGAA 735
601 CATCAGGAGCAACACCAACCAACATCTCCCTAATCTTCACTTGAGATGATTTGGA 660
736 TCCATGATCTTAGCTTTCATTA 759
661 GCCCATGAACCTTCGCTTCTTGA 684

RESULT 10
AAC55879
ID AAC55879 standard; DNA; 989 BP.
AAC55879;
25-JAN-2001 (first entry)

Eucalyptus grandis transcription factor DNA sequence #10.

KM Plant; transcription factor; gene expression; *eucalyptus*; pine; acacia;
KM poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KM basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KM homeodomain zipper; LIM domain; AP2; ERBBs; zinc finger domain;
KM type 2 Cys2His2; CCAT box element; MYB; 88.
XX *Eucalyptus grandis*.
OS
XX
PN WO200053724-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000MO-US006112.
XX
PR 11-MAR-1999; 99US-00266513.
XX 18-AUG-1999; 99US-0149485P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Wood M, McGrath A, Shenk MA, Glenn M;
XX
DR WPI; 2000-579369/54.
XX
PT New isolated polynucleotide encoding a plant transcription factor for
XX producing a plant e.g. a woody plant, preferably *eucalyptus* or pine,
XX having modified gene expression or modified activity of a polypeptide.
XX
PS Claim 1; Page 46-47; 747pp; English.
XX
CC The present invention relates to novel plant transcription factors from
XX *Eucalyptus grandis* or *Pinus radiata*. The present sequence is the coding
XX sequence for one such transcription factor. The transcription factor may
XX be used to produce a plant having modified gene expression such as a
XX woody plant e.g. a *eucalyptus*, pine, acacia, poplar, sweetgum, teak, or
XX mahogany species or to modify the activity of a polypeptide in a plant.
XX The transcription factors of the present invention are members from the

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PR	05-AUG-1999	99US-0147192P
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PR	23-AUG-1999	99US-0149930P
PR	25-AUG-1999	99US-0150566P
PR	26-AUG-1999	99US-0150884P
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PR 26-OCT-1999; 99US-0161361P
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PR 28-OCT-1999; 99US-0161992P
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PR 29-OCT-1999; 99US-0162142P

Query Match	23.4%	Score 214.4;	DB 3;	Length 954;
Best Local Similarity	61.4%	Pred. No. 7.4e-45;		
Matches 344;	Conservative	0;	Mismatches 216;	Indels 0;
				Gaps 0;

QY 49 AACACGGGAGAACACGGGAGAGAGATCGGGAGCATAGACATAAAAAAGATA 108
||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 AAAAAGATTAAACAAGAGAGAAGTAATGCGAAGGGAATCCAGATCAAGAGATA 61

109 GAGAA TCCGACGAACGCGCAATTACATATTCTAAGAGAGAGTGGATCTCGAAGA 168
 63 GGAACCTAGACAAATGACCAAGTACCTATTCAAGGAGAGAAATGTTATTTCAGGAA 121

169 GCCAAGAGCTCACCTTCTGTGATGCTCAGTCTTCATCATGTTCTCAAGACA 228

229 GGAAAGTGGCTGATTAAGCCCTTACTGATTTAAGGGGATATATGAGGTAC 288

Db 182 AACAGCTTCATGAGTATATCAGCCCTAACACCAACAGAGGAGATCGATCCTGAC 294
Qy 289 CAGGTTGTGACTGGAATGGATCTATGGAATGCTCACTATGAGAGATCAGATAACGCTG 348

Db 242 CAAACTATTCTGATGTCGATGTTTGGGCCACTCMAATATGACGGAATSCAAGAAACCAAG 30

Qy 349 AAGCATTGTAATGAGATTAAACCAAAACCTGAGGAGGAGATTAGCAGAGGAAAGGGGAG 40

Db 302 AGGAACTGTTGAGACAAATAGAAATCTCCGGACTCAGATCAAGAGGCTTAGGTGAG 361

Oy 409 GAATTGAGGGCATGACATTAAGCACTGCCGGTCTTAGCAAACTTTGGAAGATCT 466

Db 362 TGTTCGACCGACTTGACATTCAGGAGCTGCCTCGTCTTGAAGATGAATGGAACAACCT 42

Db 422 TTCAACTCGTTCGCGAGCGCAAGTTCAATCTTTGGGAATCAGATCGAGACCAAG 48

482 AAAAGAACAAAGTCAACAGACATTCAAAAAATTCATACATGAGCTGGAATAAGA 54

QY	589	GAGGAGATCCGACTACGG	608
Db	542	GCTGAAGATCCTCACAATGG	561

RESULT 13
AAC51790

1D	AAC51750	Strandberg, DNN, 11.0 DE.
XX		
AC	AAC51790;	
XX		

DT	18-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	DNA fragment SEQ ID NO: 69758.
XX		

KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.

aa Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.

XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000: 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 01-APR-1999; 99US-0127462P.
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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PR 29-SEP-1999; 99US-0156596P.

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PR 04-OCT-1999; 99US-0157117P.
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PR 29-OCT-1999; 99US-0162142P.

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Query Match 23.3%; Score 213.8; DB 3; Length 1170;
 Best Local Similarity 60.3%; Pred. No. 1.1e-44;
 Matches 353; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

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QY 24 AAGAGAGGGTGTGGAACAGAGGAAACAGGGAGAGAGAGAGATGGGAG 83
DB 201 AAGGAAAGGTCCATTAAGCCAAAGTACTTTTGACAGTGTGAGAGAAATATGGGAG 260
QY 84 GGGGAGATGAGATTAAGAAAGATAGAGATCCGACGAAAGAGAGATTAATTTCA 143
DB 261 AGGAGAGTTCAGATCAAGAGATAGAGACCAAGACAAAGACAGATGATTTCAA 320
QY 144 GAGAGAGTGGGATCTGAAGAAAGCCAGAGAGCTCATGTTCTCTGTATGCTCAGGT 203
DB 321 GAGAAAGAAATGGTTATTCAGAAAGACATGAGCTCACGGTTTGTGTATGCTAGGGT 380
QY 204 CTCTCTCATGTTCTCAAGACAGAAAGTGGCTGATTAAGTCAAGCCCTTACTGA 263
DB 381 TTGATTAATCAAGTCTCTAGCTCAACAGGTTGATGATATCAAGCCCTTAACACAC 440
QY 264 TATTAGGGGATATATGAGAGTACCAAGTGTGACTGAAATGATCTATGAAATGCTCA 323
DB 441 AACAGAGAGATTCGATGATCTGTACCAAACTATTTCTGATGTCATGTTGGGCACTCA 500
QY 324 GTATAGAGATGACGAATAGCTGAGCATCTGATGATTAACAAACCTGAGGA 383
DB 501 ATATAGCGAAATGCAAGAAACCAAGAGAAACTGTTGAGACAAATAGAAATCTCCGAC 560
QY 384 GGAGTTTGGAGAGAGAGGGGAGAAATGGAGGGAGTCAGCAATAAAGCAACTGCGGG 443
DB 561 TCAGATCAAGCAGAGGCTTAGTGTGTTTGGACAGCTTGACATTCGAGACTCGCTCG 620
QY 444 TCTTAGCAAACTTTGGAAGTCTCTTAGAATTTGAGCATAGAAAGTATCATGTGAT 503
DB 621 TCTTAGAGATGAAGTGAAGAAACACTTTCAACTCGTTGCGGAGCCAAAGTTCAATCTCT 680
QY 504 CGCCACAACTGACCTTACAGAAAGAAAGCTTTAAAGACACAGGAAATTTACCGGCG 563

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DB 681 TGGGATCAGATGACAGACCAAGAAAAAGAAACAAAGTCAACAGACATACAAAGAA 740
QY 564 TCTAATACATGAACCTGAGATATGAAGAGAGATCCGAATCAGG 608
DB 741 TCTCATACATGAGCTGAACTGAAGACTGAAGATCTCTACTATGG 785

RESULT 14
ADO61550
ADO61550 standard; DNA; 988 BP.
XX
XX ADO61550;
AC
XX 15-JUL-2004 (first entry)
DT
XX
DE Transcription factor G133 coding sequence, SEQ ID 17.
XX
XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
XX osmotic stress tolerance; cold tolerance; heat tolerance;
XX low nitrogen tolerance; low phosphate tolerance; fungal disease;
XX glyphosate resistance; flowering; fertility; seed development; ds.
XX
XX Arabidopsis thaliana.
OS
XX
XX W02004031349-A2.
PN
XX
XX 15-APR-2004.
PD
XX
XX 18-SEP-2003; 2003WO-US030292.
PF
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XX 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434166P.
PR 24-APR-2003; 2003US-0465809P.
XX
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA
XX
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TJ;
PI Kiechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;
XX
XX WPI; 2004-330163/30.
DR
XX
XX P-PSDB; ADO61551.
PT
XX
XX New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PS properties compared to a reference plant.
XX
XX Claim 1; SEQ ID NO 17; 510pp; English.
XX
XX The present invention relates to novel plant transcription factor
XX proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
XX sequences can be used to produce transgenic plants, which overexpress
XX (II), where the transgenic plant has an altered trait as compared to a
XX non-transgenic plant or wild-type plant. The transgenic plant comprises
XX an altered trait selected from increased tolerance to abiotic stress,
XX increased tolerance to osmotic stress, increased tolerance to cold,
XX increased germination in cold, increased tolerance to heat, increased
XX germination in heat, increased tolerance to freezing conditions,
XX increased tolerance to low nitrogen conditions, increased tolerance to
XX low phosphate conditions, increased tolerance to disease, including
XX fungal disease and particularly Erysiphe, Fusarium and Botrytis,
XX increased tolerance to multiple fungal pathogens, increased resistance to
XX glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
XX increased sensitivity to ACC, altered sugar sensing, increased tolerance
XX to sugars, altered carbon/nitrogen sensing, early flowering, late
XX flowering, altered flower structure, loss of flower determinacy, reduced
XX fertility, altered shoot meristem development, altered branching pattern,
XX altered stem morphology, altered vascular tissue structure, reduced
XX apical dominance, altered trichome density, altered trichome development,
XX altered trichome structure, altered root development, altered shade
XX avoidance, altered seed development, altered seed ripening, altered seed
XX germination, slow growth, fast growth, altered cell differentiation,
XX altered cell proliferation, altered cell expansion, altered phase change,
XX altered senescence, abnormal embryo development, altered programmed cell

```

CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedling, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or grey leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 988 BP; 326 A; 194 C; 202 G; 266 T; 0 U; 0 Other;

Query Match 23.2%; Score 213.2; DB 12; Length 988;

Best Local Similarly 61.2%; Pred. No. 1.5e-44;

Matches 344; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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Qy 107 TAGAGATCCGACGACAGCAAGTACATATTTAAAGAGAGATTGGATACAGAGA 166

Db 68 TAGAGACACAGACAAACAGCAAGTACATTTCAAGAGAGAGATGGTTATTCAAGA 127

Qy 167 AGCCCAAGAGACTACGTTCTCTGTGATGTCAGGTCCTCTCATATGTTTCAGACA 226

Db 128 AAGCACATGAGCTCACGGTTTGTGTATGTAGGGTTTGCATATATCATGTTCTTACCT 187

Qy 227 CAGGAAGTTGGCTGATTAATGCGCCCTCTACTGATATTAAGGGATATATGAGAGT 286

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Qy 287 ACCAGGTTGATCGAATGATCTATGAAATGCTCAGATAGAGAGATGCAATAGC 346

Db 248 ACCAACTATTTGATGTGATGTTGGGCACTCATATGACGATGCAAGAAACA 307

Qy 347 TGAAGCATCTGAATGATTAACCAAACTGAGAGAGAGATTAAGAGAGAGAGGGG 406

Db 308 AGAGGAACTGTTGAGAGCAAAATAGAAATCCGCACTCAGATCAACAGAGCTAGGTG 367

Qy 407 AGGAATGAGAGGATGAGCAATAAGCAACTGCGCGCTTGAACAACTTGGAGAGT 466

Db 368 AGTGTGAGACGACTTGACATTGAGAGCTGCGTCTTGGAGAGAGAGAGAAACA 427

Qy 467 CTCTTAGAATTTGATGATGAGAAATATCATGATGCGCCACAACACTGACATTACA 526

Db 428 CTTTCAAACTGTTGCGAGAGGCAAGTTCAAAATCTTTGGGAATCAATGAGACACA 487

Qy 527 AGAAAAAGCTTAAAGACAGAGGAACTTACCGCGCTTAAATCATGAATGATATGA 586

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Qy 587 AAGAGAGATCGAATACGG 608

Db 548 GAGCTGAAGATCTCATATAG 569

RESULT 15

AAC40831 ID AAC40831 standard; DNA; 959 BP.

XX AAC40831;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29696.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

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XX 05-MAR-1999; 99US-01223180P.

XX 09-MAR-1999; 99US-0123548P.

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 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
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 PR 29-OCT-1999; 99US-0162142P.

Query Match 23.1%; Score 211.6; DB 3; Length 959;
 Best Local Similarity 61.0%; Pred. No. 3.9e-44;
 Matches 343; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY 47 AAAACAGGGAGAACAGGGAGAGAGATGGGGAGGGAGATGAGATTAAGAA 106
 DB 4 ACAAAAAGATTAAACAAAGAGAGAGAAATATGCGAGAGGAAAGATCAGATCAAGGA 63
 QY 107 TAGGATCCGAGAAACAGCAAGTTACATATTCTAAGAGAGATTGGACTGAGA 166
 DB 64 TAGAGAACCAAGAACCAAGACAGACAGTACATTCAAGAGAAAGATGTTATTCAAG 123
 QY 167 AGGCAAGAGACTCACTGTTCTCTGTGATGCTCAGTCTCTCATCATGTTTCAAGCA 226
 DB 124 AAGCAATGAGCTCAGCGTTTGTGTGATGCTGAGGTTTGATATCATGTTCTTACGT 183
 QY 227 CAGGAAGTTGGCTGATTACTGACGCCCTTACTATATTAAGGGATATATGAGAGT 286
 DB 184 CCAACAACTTCAGATATATATACGCCCTTAACACCAACAAAGAGAGATGTATATCTGT 243
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Db	424	CTTCAAACTCGTTGCGGAGCGCAAGTTCAAACTCTTGGGAAATCAGATCGAGCCACCA	483
Qy	527	AGAAAAAGCTTAAAGCACAGGAAACTTACCGCGCTCTAATACATGAATGATATGA	586
Db	484	AGAAAAAGAACAAAGTCAACAGACATACAAAAGAAATCTCATACATGAGCTGGAATTA	543
Qy	587	AAGAGGAATCCGAATCTACGG	608
Db	544	GAGCTGAAGATCCTCCTACTATGG	565

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 Job time : 626 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:04:32 ; Search time 3732 Seconds
(without alignments)
9352.876 Million cell updates/sec

Title: US-10-690-246A-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	255.2	27.8	692	6	CB972246 CAB10006_
5	250.8	27.4	694	6	CB921382 VYD070D08
6	246	26.8	651	5	BU994760 HM08C02r
7	245.8	26.3	591	7	CO955351 eca01-5cs
8	241.6	26.3	650	7	CV005022 eca01-13c
9	238.6	26.0	645	2	BA97689 WHE955.D0
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ALIGNMENTS

RESULT 1
LOCUS CO997489 615 bp mRNA linear
DEFINITION ltu01-6m61-e12 ltu01 Liriodendron tulipifera cDNA clone
1tu01-6m61-e12 5', mRNA sequence.

ACCESSION CO997489
VERSION CO997489.1 GI:51356713
KEYWORDS EST.
SOURCE Liriodendron tulipifera
ORGANISM Liriodendron tulipifera

REFERENCE

dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
Lebens-Mack, J., Landherr, L., Schlarbaum, S., Ilut, D. and Wall, K.
1 (bases 1 to 615)
Generation of ESTs from early flower buds of Liriodendron
tulipifera

JOURNAL

COMMENT Unpublished (2003)
Contact: Claude dePamphilis or James Lebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131

FEATURES
source
Email: cw43@psu.edu or jh110@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: ltu01-6m61 row: e column: 12
Seq primer: M13F.
Location/Qualifiers
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/organism="Liriodendron tulipifera"
/mol_type="mRNA"
/db_xref="taxon:3415"
/clone="ltu01-6m61-e12"
/issue_type="flower buds"
/dev_stage="1-35 mm buds"
/lab_host="SOAR"
/clone_id="ltu01"
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; This is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

rosids; Vitaceae; Vitis.
1 (bases 1 to 762)
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
Jones, K. and Cook, D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcoc@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers

FEATURES
source

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1. 762
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10005_Ia_Fa_B07"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom"
/lab_host="DHSalpha"
/clone_id="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1:
SfiI; Site_2: SfiI; CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calypters or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGCAGGTGATCAACGAGAGTGCGCATTAACGCCGGG-3' and
5'-ATTCTAGAGCGCGGCGGCGGACATG-DT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
```

ORIGIN

Query Match 28.1%; Score 257.8; DB 6; Length 762;

Best Local Similarity 67.3%; Pred. No. 6.9e-51;

Matches 364; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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68 AGAAGAGATGGGAGGGGGAAGATAGATTAAGAAAGGCCAAGAGCTCACTTTC
2 AGGAGGTGATGCTAGAGAAAGATTGATCAAGAGATAGAACTCGACGAACAGGC
128 AAGTTACATATTTCAAGAGAGTTGGGATCTGAAGAGGCCAAGAGCTCACTTTC
62 AGGTCACTTACTCCAGAGAGAAATGATCTTCAAGAAAGCCAGTAGCTCACTGTTTC
188 TCTGTGATGCTCAAGGTCTCTCATCATGTTTCTCAAGCAAGAAAGTTGGCTGATTA
122 TTTGTGATGCTAAGGTTTCTATCATCATGCTCTCCAGTACGAAAGCTCCATGAATCA
248 GCAAGCCCTTACTGATATTAAGGGGATATAGAGGTACAGGTTGTGACTGGAATGG
182 TCAGGCCCTTCCATCAAGAAACAAATATTGATCACTACCAACCACTTAGAGAGTGG
308 ATTATGGAATGCTCATGATAGAGAGATGCAAGATACCTGGAAGCATCTGAATGATTA
242 ATCTATGAGATATCACTATGAGAGAAATGCAAGAAACCTGAAGAAATGGAATGGA
368 ACCAAACCTGAGAGAGAGATTAGAGAGAGAGAGAGAGAGATTTGAGAGGCTGACA
302 ACAAGATCTCAGAGAGAGATTAGAGAGAGATGGGTGAACATTTGAGCCGATTGAGCG
428 TTAAGCAATGGCGGCTTTGAGCAAACTTTGGAAGAGTCTTTAGATTTGTTAGCACTA
362 TTGAGAACTGCGAGATCTTGAACAAAGATGAGAGAGTTCTTTGAAGAGTTCCTGATA
```

QY 488 GAAGTATCATGTGATCGCCACAAACTGACACTTACAAAGAAAGCTTAAGACAA 547
DB 422 GGAGTACACAGGAGTAAATATCATGATTGAAATCTTCAAGAAAGCTTAGAAGATGG 481
QY 548 GGAAGACTTACCGGCTTATATCATGAACTGATATGAAGAGAAATCCCACTAGC 607
DB 482 AACAAATACAAAAATCTCTACATGAAATTGATGACAGGACAGAGATCATATCTATG 541
QY 608 G 608
DB 542 G 542

RESULT 4
CB972246 692 bp mRNA linear EST 30-APR-2003
LOCUS CAB10006_Ia_Fa_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 Vitis
DEFINITION vinifera cDNA clone CAB10006_Ia_Fa_D07 5', mRNA sequence.
ACCESSION CB972246 GI:30256403
VERSION CB972246
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 692)
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
Jones, K. and Cook, D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcoc@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

```
1. 692
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10006_Ia_Fa_D07"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom"
/lab_host="DHSalpha"
/clone_id="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1:
SfiI; Site_2: SfiI; CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calypters or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGCAGGTGATCAACGAGAGTGCGCATTAACGCCGGG-3' and
5'-ATTCTAGAGCGGCGGCGGCGGACATG-DT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
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ORIGIN

Query Match 27.8%; Score 255.2; DB 6; Length 692;

Best Local Similarity 65.4%; Pred. No. 2.9e-50;

Matches 374; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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QY 37 AGAACAGAGAAACAGGCGAGAAACAGGCGAAGAGAGATGGGAGGCGGAAGATAGAG 96
```

```
Db      12 AGAAGGATCTGGAATCGAGGAGAGAGAGGATGCTAGAGGAAAGATTGAG 71
Qy      97 ATAAAAAAGATAGAGATCCGACGAAACAGGCAAGTTATCATATTCTAAAGAGAGATTGGG 156
Db      72 ATCAAAAGATAGAGACTCGACGAAACAGGCAAGTCACTTCCAAAGAGACGAATGTGT 131
Qy      157 ATACAGAGAGGCGAAGAGCTCAGTGTCTCTGTGATGCTCAGAGTCTCTCATCATG 216
Db      132 ATCTTCAAGAGGCGAGTGAAGTCACTGTTCTTTGTGATGCTAAGTTCTATCATCATG 191
Qy      217 TTCTCAAGCAAGAAAGTTGCGATTACTGACGCCCTCTATCATATTAAAGGAGATA 276
Db      192 CTCTCAGATAGTGAAGAGCTCCATGAATACATCAGCCCTTCCACTCAACGAAACAAAT 251
Qy      277 TATGAGAGTACCAAGTTGTGACTGATGATCTATGATCTCAATCTCAATGAGAGATG 336
Db      252 TTGTTCAGTACCAAGACACTCTAGGAGTGGATCTATGAGCTATCATATGAGAGATG 311
Qy      337 CAGAAATACGCTGAAGATCTGAATGATTAATTAACAAACCTGAGAGAGAGATTAGAGAG 396
Db      312 CAGAAAGAACTTGAAGAACTGAAAGATGTGAACAAGATTCAGAGAGAGATTAGGAG 371
Qy      397 AGGAAGGAGAGATTTGAGGCAATGACATTAAGCAACTGCGCGCTTTGAGCAAACT 456
Db      372 AGGATGGGTGAACATTTGAGCGATTTGAGCGTTGAGGAATCGGAGATCTTGAACAAG 431
Qy      457 TTGGAAGAGTCTTGAATTTGTTAGCATAGAAAGTATCATGTATCGCACAAACT 516
Db      432 ATGAGAGTCTTTGAAGATGTTGATGATGAGATGAGATCAATTAATTCAGATT 491
Qy      517 GACACTTACAGAAAGTTAAAGCAAAAGGAACTTACCGCGCTCTAATACATGAA 576
Db      492 GAAACTTTCAAGAAAGCGTGAAGATGTGGAACAAATATCAAAATCTCTCATGAA 551
Qy      577 CTGATATGAAAGAGAGAACTCGAACTACGG 608
Db      552 TTGTATGCAAGGACAGAGATCAATCTATAG 583

RESULT 5
CB921382 694 bp mRNA linear EST 25-APR-2003
LOCUS    VVD070D08.353397 An expressed sequence tag database for abiotic
DEFINITION
stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVD070D08.5, mRNA sequence.
CB921382
CB921382.1 GI:30136044
EST.
SOURCE   Vitis vinifera
ORGANISM Vitis vinifera
Bukariyoti; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 694)
Cushman, J.C.
An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMER
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 070 row: D column: 08
Seq primer: T3 20mer
High quality sequence stop: 694.
Location/Qualifiers
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1..694
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD070D08"
/tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_1fb="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: lambda uni-zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Query Match 27.4%; Score 250.8; DB 6; Length 694;
Best local Similarity 61.3%; Pred. No. 3.3e-49;
Matches 424; Conservative 0; Mismatches 262; Indels 6; Gaps 1;

Qy      79 GGAAGGGGAGATAGATTAATAAAGATAGAAATCCGACGAAACGCAAGTTCATAT 138
Db      1 GGTCTGGGAAATTTGAGATCAAGAGATAGAAACCCACCAAGAGCGAGTCACTAC 60
Qy      139 TCTAAGAGAGACTTGGATCTGAAGAGCGCAAGAGCTCACTGTTCTGTGATGCT 198
Db      61 TCCAGCGACGAAATGATTTTCAAGAAAGCCAGAGCTCACGTTCTTTGTATGCT 120
Qy      199 CAGGCTCTCTCATCATGTTCTCAAGCACAGGAAAGTTGGCTGATTAATCTGACGCCCTCT 258
Db      121 AAGTTTCACTCATCATATGTTCTCAATCTGAAATTCAGGAATATACAGTCTACT 180
Qy      259 ACTGATATTAAAGGGATATATGAGAGTACCGAGTTGTGATGGAATGATCTTAGAAT 318
Db      181 ATTAACACGAAAAAGGCTTACATCATCATGATCAAGAACTTTGAGGATGATCTTTGGAC 240
Qy      319 GCTCGATAGAGAGATGAGAAATACGCTGAAGCATCTGAATGATTAACAAACCTG 378
Db      241 TCTCACTAGAGAGATGCAAGAAACCTTGCAAAACGTAAGAGATCAACAACAATTA 300
Qy      379 AGGAAGAGATTTAGAGAGAGGAGAGATTTGAGGAGATGACATTAAGCAACTG 438
Db      301 AGGAGAGATCAAGGAAAGATGGGTGAAGATTTGGGAGATCTGAGATTTAGGAGCTG 360
Qy      439 CCGGCTCTTGAAGAACTTTGAGAGAGTCTTGAATGTTAGGATGAAGAAATGAT 498
Db      361 CCGGCGCTTGAAGAGAGATGAGACGCTCTTTAGGATTTAGTACGCAAGGAAATGAC 420
Qy      499 GTGATGCCACCAACCTGACCTTACAGAAAGCTTAAAGCAACAGGAACTTAC 558
Db      421 GTGATCAAAACTGACCGAGACCTACAGAAAGGTCAGAACTTGAAGAACACAC 480
Qy      559 CCGGCTCTAATCATGAACTGATATGAAGAGAGAAATCCGAATCAAGTTTAAATGA 618
Db      481 GGAATCTCTCTCTCAACTTTGAGGCAAAATGCAATGATCCACTTACAGAT-----TA 534
Qy      619 GAAACCAAGATAGAAATTTATGAAATTTGATTCATGATGTAAGATGTCTCATGATG 678
Db      535 GTGAAATAAGATGAGATATGATCATGACGGTGGCAATTTGCAAAACGGGCTTCAACCTC 594
Qy      679 TTTTCTTTAGGTTGTTGATCGAATGAGCCCAATCTGCTGTTAGTTATGAATGA 738
Db      595 TATGCTTTGCTGCTGATGAGGCCCACTTAATCTTACACATGATGGGGAATATGATCA 654
Qy      739 CATGATCTTAGCCTTGCAATATGAGCAATAT 770
Db      655 CATGATCTGCGCTTCTGATCATGATGCAAT 686

RESULT 6
BU994760 651 bp mRNA linear EST 23-OCT-2002
LOCUS    HM08C02 HM Hordeum vulgare subsp. vulgare CDNA clone HM08C02
DEFINITION
5-PRIME, mRNA sequence.
ACCESSION
BU994760
BU994760.1 GI:24271743
```


[illegible]

Full sequence and original trace file are available from the Plant Genome Network website (<http://pgn.cornell.edu>)

Plate: eca01-13c83 row: d column: 12

Seq primer: M13F.

Location/Qualifiers

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1. 650
  /organism="Eichscholzia californica"
  /mol_type="rRNA"
  /cultivar="Aurantiflora Orange"
  /db_xref="taxon:3467"
  /clone="eca01-13c83-d12"
  /rissue_type="flower buds <= 2.5mm"
  /dev_stage="millimeter buds"
  /lab_host="SOLR"
  /clone_idb="Eca01"
  /note="Vector: pBluescript SK (+/-); Site_1: EcoRI;
  Site_2: XhoI; Plants were grown in greenhouse at Penn
  State from commercially available seeds. Only floral buds
  with diameter of 2.5 mm or less were collected. This is a
  directionally cloned, non-normalized library. Avg. insert
  length: 1702; Primers: M13F and M13R; Antibiotic: 50 ug/ml
  Ampicillin; Primary titer: 785 pln total; Amplified titer:
  1.68E11 pfu/ml; Mass Excised titer: 5.6E8 total; This
  library has been generated by the Floral Genome Project
  (FGP). We would like to thank Huck Life Sciences
  Consortium for their assistance. The Floral Genome Project
  is funded by NSF's Plant Genome Research Program
  (DBI-0115684). More information about the project can be
  obtained at http://fgrp.bio.psu.edu"
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ORIGIN

Query Match	26.3%	Score 241.6	DB 7	Length 650
Beet Local Similarity	67.9%	Pred. No. 5.4e-47		
Matches 337	Conserve	0	Mismatches 159	Indels 0
Gaps				0
QY	85	GGGAAAGTATGAGTATTAAGTATGAGATTCGACGAAACAGGCAAGTATCATATTTCTAAG	144	
DB	1	GGAAAGTATGAGTATTAAGTATGAGATTCGACGAAACAGGCAAGTATCATATTTCTAAG	60	
QY	145	AGGAGAGTGGGATATCTGAAGAAAGCCAGAGAGCTCACTGTTCTGTGATGCTCAGGTC	204	
DB	61	AGAGAGAGTGGATATTAAGAAAGAGCTCGAGTATCACTGTTCTGTGATGCTCAGGTC	120	
QY	205	TCTCTCATGTTTCTCAAGCAGAGAAAGTTGGCTGATTAATGACGACCCCTCTACATGAT	264	
DB	121	TCACCTATATATGTTCTCACTACGAGAAATTTCTGAAATATATCAAGTCTTCTGTTTCG	180	
QY	265	ATTAAAGGAGATATATGAGAGATACCAAGTTGTGACTGGAATGATCTATGGAATGCTCAG	324	
DB	181	ACAAAGAGAGATATATGATCGATATCAACAGTTTCAAGAACTATTTCTGGAATTTCTAC	240	
QY	325	TATGAGAGATATGAGATATACGCTGAGACATCTGATATGATATTAACAAACCTGAGAG	384	
DB	241	TACAGAGTTTGCAGAAATTAATTGAAACAGAGATGAGATTAACATATAGCTCCGAGA	300	
QY	385	GAGATATGAGAGAGAAAGGGGAGAAATTTGAGGGCCTGGAATTAAGCAATCTGCGGCT	444	
DB	301	GAAATTTAGACAGAGATGAGAGAGATTTGGATGATCTGAGCAGCAATGAACTTTCAGAT	360	
QY	445	CTTGAAGCAATTTGGAAGAGCTCTTGAATTTGATGAGATGAAATGATCATGTATC	504	
DB	361	CTTGAAGCAATTTGGAAGAGCTCTTGAAGTTGTTGATGAGCAAGATATCATGTATTT	420	
QY	505	GCCACAGAACTGACATTAACAAGAAACCTTAAAGCAACAGGAGAACTTACCGGCT	564	
DB	421	AGTACTAGTCTGACATATCAAGAAAAATTAAGAACCAAGCAAGCAATCAATTAAT	480	
QY	565	CTAATATCATGAACTGG	580	
DB	481	CTCCTGCTGGAATTTG	496	

RESULT 9

BE497689 645 bp mRNA linear EST 04-AUG-2000
 LOCUS BE497689
 DEFINITION WHE955_D02_G0325 Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE955_D02_G03, mRNA sequence.
 ACCESSION BE497689
 VERSION BE497689.1 GI:9696306
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 645)
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsieh, C.C., Kang, Y., Lazo, G.R., Miller, R., Raushch, C.J., Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
 Unpublished (2000)
 JOURNAL Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
 Seq primer: Stragene SK primer.
 FEATURES
 source
 1..645
 location/Qualifiers
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE955_D02_G03"
 /issue_type="Spike before anthesis"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /clone_lib="Wheat pre-anthesis spike cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

Db 345 TGAATCGACGATGATAGATATATGACGCCACGCTGAGCATTCAGACATCAATCCG 404
 Qy 373 AACCTGAGGAAGAGATTGAGAGAGAAAGGGAGAAATTGGAGGCAATGACATTAAG 432
 Db 405 AACCTGCGGACCGAGAT-----CAGATGGGTGAAGATCTGACCGCGGTTCGAG 458
 Qy 433 CAACCTGCGGCTTTTGAAGCAAACTTTGGAAGACTCTTGAATTTGTTAGGCAATGAAG 492
 Db 459 GACCTGCGGACCTTGAAGCAAAATGTCAGTCCGCTCTCAAGAGATTCCGAGAGAG 518
 Qy 493 TATCATGTGATCGCCACACAACTGACACTTACAAAGAAAGCTTAAAGCAGAGGAA 552
 Db 519 TATCATGTGATCAACGACGAGCTGAAACCTTACAAAGAGGTGAAGCACTCCAGAG 578
 Qy 553 ACTTACCGCGCTCTTAATACATGAACTGATATGAAGAGAGAAATCCGAG 603
 Db 579 GCATACAAAGATCTGCGAGGAGCTGGTATGCGGAGGACCGGCGTAC 629
 RESULT 10
 CA732396 605 bp mRNA linear EST 26-NOV-2002
 LOCUS CA732396
 DEFINITION wipic.pk005.m21 wipic Triticum aestivum cDNA clone wipic.pk005.m21 5' end, mRNA sequence.
 ACCESSION CA732396
 VERSION CA732396.1 GI:25547994
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 605)
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Mao, G., Caraher, N. and Hanafey, M.K.
 Dupont Wheat cDNA Sequence
 Unpublished (2002)
 JOURNAL Contact: Scott V. Tingey
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@USA.dupont.com
 Seq primer: M13.
 FEATURES
 source
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 location/Qualifiers
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wipic.pk005.m21"
 /issue_type="lemma and palea"
 /lab_host="DH108"
 /clone_lib="wipic"
 /note="Vector: plasmid SK; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum, Hi line) lemma and palea"

ORIGIN
 Query Match 25.9%; Score 237.8; DB 6; Length 605;
 Best Local Similarity 67.7%; Pred. No. 4.1e-46;
 Matches 329; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Db 73 GAGATGGGAGGGGAGATAGATATAAAGATAGATTCGACGAACAGCAAGTT 132
 Qy 111 GAGATGGGCGGGGAGATGATGATTAAGGATCGAGAAAGCGCAACAGCAAGTTG 170
 Db 133 ACATATTCTAAGAGAGATTGGATCTGAAGAAAGCCAAAGAGCTCACTGTTCTCTGT 192
 Qy 171 ACCTACTCAAGCCCGCTCGGGATCATGAAAGAGCGCGGAGCTCACGTCCTGTC 230
 Db 193 GATGCTAGGCTCTCATCATGTTCTCAAGCAAGAAAGTTGGCTGATTAATGACG 252
 Qy 313 TGAATGCTCAGTATGAGAGATGCAAGATACGTGAAGCATCTGAATGATTAACCA 372

Db 231 GAGCCAGGTGCGCATCATCATGTTCTCTCCACCGGCAAGTACCAAGATTCTGACG 290
 Qy 253 CCTCTACTGATATTAAAGGGGATATATGAGAGTACCAGTTGTGACTGAAATGATCTA 312
 Db 291 ACCGGACCGACATCAAGGGGATCTTTGACCGCTTACGAGGCGCATCGGACACCGTG 350
 Qy 313 TGGATGTCTGATGATGAGAGATGAGAAATACGCTGAGATCTGATGATTAACAA 372
 Db 351 TGGATGAGCAGATATGAGATATGACGCGACCGCTGACCATCTTCAAGACATCAATCG 410
 Qy 373 AACCTGAGAAAGAGATTGAGAGAGAAAGGGGAGAAATTTGAGGGCATGACATPAAG 432
 Db 411 AACCTGCGACCGAGATCAGGCAAGAGATGGGTGAAGATCTGGACGCGCTGAGTTGAG 470
 Qy 433 CAACCTGCGGCTTTGAGCAAACTTTGAGAGAGTCTTTGATTTGTAGGCAATGAAAG 492
 Db 471 GAGCTCGCGACCTTTGAAACAAATGTCAGATGCGCTCTCAAGAGATCGCCGAGNNNAG 530
 Qy 493 TATCATGTGATCGCCACACAACTGACACTTACAGAAAGGCTTAAAGCACAGGAA 552
 Db 531 TATCATGTGATCAACGACGACGACTGAACCTACAGAAAGGTGAAGCATCTCCANNAG 590
 Qy 553 ACTTAC 558
 Db 591 GCATAC 596
 RESULT 11 532 bp mRNA linear EST 17-NOV-2000
 LOCUS BF291839
 DEFINITION WHE2204_E12_J24Zs Aegilops speltoides anther cDNA library Aegilops
 ACCESSION BF291839
 VERSION BF291839.1 GI:11222903
 KEYWORDS EST.
 SOURCE Aegilops speltoides
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Aegilops.
 1 (bases 1 to 532)
 Ahniov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J.,
 Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P., Iazo, G.R.,
 Miller, R., Otto, C., Rausch, C.J., Seaton, C.L., Simons, K., Tong, J.C.
 and Zhang, D.
 The structure and function of the expressed portion of the wheat
 genomes - Anther cDNA library from Aegilops speltoides
 Contact: Olin Anderson
 Unpublished (2000)
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: canderan@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low
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 Seq primer: StrataGene SK primer.
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 chamber at the University of California, Davis (Ahniov)."

ORIGIN
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 Best Local Similarity 69.9%; Pred. No. 5.6e-46;
 Matches 320; Conservative 0; Mismatches 138; Indels 0; Gaps 0;
 Premiotic anthers were harvested, total RNA and poly(A)
 RNA were prepared, from each tissue and then pooled. A
 cDNA library was made, and the cDNA clones were in vivo
 excised to give pBluescript phagemids in the T3 Close lab
 (Ahniov, Chin, Choi, Close, Fenton, Kianian, Otto,
 Simons, Zhang) at the University of California, Riverside.
 Plasmid DNA preparations and DNA sequencing were performed
 in the OD Anderson lab (all other authors)."
 73 GAGATGGGGAGGGGAGATAGATTAATAAAGATAGAGATCCGACAAAGCGAAGTT 132
 Db 75 GAGATGGGGAGGGGAGATAGATTAATAAAGATAGAGATCCGACAAAGCGAGTG 134
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 LOCUS CD439730
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 ACCESSION CD439730
 VERSION CD439730.1 GI:31355373
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 SOURCE Zea mays
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 872)
 Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
 Larkin, B., Beckett, P., and Messing, J.
 Characterization of the maize endosperm transcriptome and its
 comparison to the rice genome
 Genome Res. 14 (10), 1932-1937 (2004)
 Contact: Lai, Jinheng
 Dr. Joachim Messing's lab
 Wakeman Institute, Rutgers University
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
 Tel: 732-445-3801
 Fax: 732-445-3801
 Email: jlai@wakeman.rutgers.edu
 Seq primer: T3.

FEATURES

source

Location/Qualifiers

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735 ATCAATGATTTTGGCTTGCATA 758
802 CTTCCAGAGCTTCGCGCTGGGCTA 825

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 ACCESSION AY109302
 VERSION AY109302.1 GI:21212794
 KEYWORDS HTC.
 SOURCE Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 1273)

AUTHORS

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., White, M.S.,

TITLE

Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.

JOURNAL

Maize Mapping Project/DuPont Consensus Sequences for Design of

REFERENCE

Unpublished (2002)

AUTHORS

Coe, S.H.

TITLE

Direct Submission

JOURNAL

Submitted (25-APR-2002) Maize Mapping Project, University of

COMMENT

Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MBL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES

source

Location/Qualifiers

1..1273

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Library"

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assemblies resulting from the application of public

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assembled by DuPont as part of a collaboration for the

overgo addressing of BACs in conjunction with the Maize

Mapping Project"

ORIGIN

Query Match 25.7%; Score 236; DB 3; Length 1273;
 Best Local Similarity 59.1%; Pred. No. 1.3e-45;
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206 CTACTCCAGCGCGCGGAGATCAAGAAAGGCGCGAGCTCAACCGTCTCGA 265
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ACCESSION CAS97172
VERSION CAS97172.1 GI:25149628
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 605)
Tingey,S.V., Moore,G., Griffiths,S., Powell,W., Mollers,P.,
Dolan,M., Hainey,C., Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence in collaboration with the John Innes
Center 1
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
FEATURES
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XhoI; Wheat (Triticum aestivum) pre-meiotic anthers JIC"
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Best Local Similarity 66.0%; Pred. No. 7.3e-45;
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ACCESSION AJ803128
VERSION AJ803128.1 GI:51118456
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
1 (bases 1 to 604)
Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungsfor-schung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	227.2	24.8	681 3	US-09-410-464-3 Sequence 3, Appli
3	216.6	23.6	989 4	US-09-640-211A-10 Sequence 10, Appli
4	159.2	17.4	386 4	US-09-640-211A-2008 Sequence 2008, Ap
5	149.8	16.3	905 4	US-09-640-211A-1944 Sequence 1944, Ap
6	143.4	15.6	409 4	US-09-640-211A-1512 Sequence 1512, Ap
7	124	13.5	263 4	US-09-640-211A-1476 Sequence 1476, Ap
8	116	12.6	613 4	US-09-640-211A-2019 Sequence 2019, Ap
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10	109.2	11.9	412 4	US-09-640-211A-2031 Sequence 2031, Ap
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12	105.8	11.5	396 4	US-09-640-211A-1490 Sequence 1490, Ap
13	102.8	11.2	475 4	US-09-640-211A-1952 Sequence 1952, Ap
14	102.8	11.2	684 4	US-09-640-211A-69 Sequence 69, Appli
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16	102.2	11.1	356 4	US-09-640-211A-2017 Sequence 2017, Ap
17	101.8	11.1	1180 2	US-08-867-087B-16 Sequence 16, Appli
18	101.2	11.0	5131 4	US-09-853-450-43 Sequence 43, Appli
19	98.6	10.8	479 4	US-09-640-211A-350 Sequence 350, App
20	98.6	10.8	479 4	US-09-640-211A-2091 Sequence 2091, Ap
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24	97.4	10.6	749 4	US-09-640-211A-1980 Sequence 1980, Ap
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32	95.4	10.4	5070 4	US-09-853-450-44 Sequence 44, Appli
33	95.4	10.4	5171 4	US-09-853-450-42 Sequence 42, Appli
34	95.2	10.4	407 4	US-09-640-211A-333 Sequence 333, App
35	95.2	10.4	407 4	US-09-640-211A-2066 Sequence 2066, Ap
36	95	10.4	2437 3	US-08-904-284-6 Sequence 368, App
37	94.4	10.3	243 4	US-09-640-211A-368 Sequence 1999, Ap
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41	93	10.1	795 3	US-08-904-284-2 Sequence 1463, Ap
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ALIGNMENTS

RESULT 1
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Sequence 2, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OR INVENTION: Floral homeotic genes for manipulation of flowering in
TITLE OR INVENTION: poplar and other plant species.
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 946
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(684)
US-09-410-464-2

Query Match 24.9%; Score 228; DB 3; Length 946;
Best local similarity 58.3%; Pred. No. 2.9e-52;
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY	76	ATGGGAGGGGAGATAGATGATTAAGATGAGATCCGAGACAGGAGTTACA	135
DB	1	ATGGGTGGTGAAGATTGAATCAAGAGATCAAAACCCAGCAAGGTCAAC	60
QY	136	TATTTAAGAGAGATGGGATCTAGAGAGCCAGAGGCTCACTGTTCTGTGAT	195
DB	61	TACTCGAAGAGAAATATGATTTTCAAGAAAGCCAGAACTCACTGATTTGAT	120
QY	196	GCTCAGGTCTCTCATCATCTTTCTCAAGCAGAGAAAGTTGCTGATTAACAGCCCC	255
DB	121	GCTAAGGTCTCTTATCATCTGTTCTCAACACTTAACAACTCAATGATTAAGCCCC	180
QY	256	TCTACTGATATTAGGGGATATTATAGAGATGACAGGTTGACTGGAATGATCTAAG	315
DB	181	TTCCATCGAAGAAAGATCTACATCATATATGAACGCTTTAGGATGATCTGTGG	240
QY	316	AATCTCAGTATGAGAGATCAGAAATACGCTGAGAGATCTGAATGATTAACCAAAAC	375
DB	241	GGCACTCATATCGAAGAAATATCAAGAGCACTTGAAGAGTGAATGATCATCATAAAG	300

Qy	376	CTAGAGAAAGGATTTTGGAGAGAGAAAGGGGAGGAATTGAGGGCATGACATTAACCA	4355
Db	301	CTGAGACAAAGTAATCGGCGAGAGAGAGAGGGGCTGAATGATCTGACATTGATCAT	360
Qy	436	CTGGCGGCTTGTAGCAAACTTTGGAGAGTCTCTTGAATTTGTAGGCATGAAAGTAT	4955
Db	361	CTGGCGGCTTGTAGCAACATATGACTGAAGCTTGAAATGGTGTGCTGGCAGGAAGTAC	420
Qy	496	CATGTGATGCCACACAAACTGACACTTTCAGAAAAAGCTTAAAGACAAAGGAACCT	5555
Db	421	CATGTGATCAAAACACAAAACGAACCTTCAGAGAAAGGTGAAGAAATTTGAGAGAGA	480
Qy	556	TACCGGCTCTAATCATGCACTGATATGAAAGAGAGAAATCCGAATCAAGCTTTTAAT	6155
Db	481	CATGGAACCTCTTGATGGAATRTAGCAAAACTAGAGATCGACGATATGTTTAGTG	540
Qy	616	GTAGAAAAACAGAGTAGAATTTATGAAATTCGATTCCAATGGTAGATGACTGTCTCAG	6795
Db	541	GACAAATGAACCTGCTGTGGCACTTGGAAATGGGGGCTTCCAACTCTATGCAATCCGGCTG	6000
Qy	676	ATGTTTTCTTTAGGGTGTTCATCCGAATCAAGCCCAATCTGCTGTGTTTAGTTTANGAA	7355
Db	601	CATCACGGGACACACACCAACCAACCATCTCCTAATCTTCACCTTGGAGATGATTTGGA	6600
Qy	736	TCAATGATCTTGAAGCTTGACATA	759
Db	661	GCCCATGAACCTGCGCTTCTCTTGA	684

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RESULT 2
US-09-410-464-3
/ Sequence 3, Application US/09410464
/ Patent No. 6395892
/ GENERAL INFORMATION:
/ APPLICANT: Straus et al.
/ TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
/ TITLE OF INVENTION: poplar and other plant species.
/ FILE REFERENCE: 53375
/ CURRENT APPLICATION NUMBER: US/09/410,464
/ EARLIER APPLICATION NUMBER: 09/267,700
/ EARLIER FILING DATE: 1999-04-06
/ EARLIER APPLICATION NUMBER: 60/080,851
/ EARLIER FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 681
/ TYPE: DNA
/ ORGANISM: Populus balsamifera subsp. trichocarpa
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(681)
US-09-410-464-3

Query Match          24.8%; Score 227.2; DB 3; Length 681;
Beet Local Similarity 58.4%; Pred. No. 46-52;
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0

QY      76  ATGGGAGGGGGAGATGAGATATAAAAAGATAGAGAAATCCGACGAACAGCGCACTTACA 135
DDB      1  ATGGGTCGTGGAAAGATGGAATCAAGAAAGATCGAAAACCCCAACAAACAGGCAAGTCAAC 60
QY      136 TATTTAAGAGAGAGTTGGGATCTGGAAGAAAGCCCAAGAGACTCACTGTTCTCTGTAT 195
DDB      61  TACTGAAAGAGAAAGAAATGATTTTCAAGAAAGCCCAAGAACTCACTGACTTTGTGAT 120
QY      196 GGTCAAGTCTCTCTATCATCTGTTCTCAAGCACAGGAAGAGTTGGCTGATTAATGCACGCC 255
DDB      121 GGTAAAGTCTCTTATATCATGTTCTTCCAAACACTAACAAACCTCAATGAGATGATGCCCC 180
QY      256 TTTACTGATATTAAAGGGATATATGAGAGGTCCAGAGTTGTACTGTGAATGGAATCTTAAG 315

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Db	181	TCACATCGACAAAAGAGTCTAGATCAATATACAAAGCTTTAGGCATAGATCTGTGG	240
Qy	316	AATGCTCAGTATGAGAGATGCAAAATACGTGAAGCATCTGAATGAGATTACCAAAAC	375
Db	241	GGCACCATTATAGAAAAATGCAAGACCTTGGAAAGCTGAATGATTCATTAAG	300
Qy	376	CTGAGAAAGAGATTAGAGAGAGAAAGGGAGAAATTGAGAGGCATGACATTAAGCAA	435
Db	301	CTGAGCAAGAAATCAGGACGAGAGAGAGAAAGGGCCGATGATGCTGAGCATTTGATCAT	360
Qy	436	CTGCGCGGCTCTTGACCAAACCTTGGAGAAGTCTCTTGAATTTGTAGGCATAGAAATAT	495
Db	361	CTGCGGGGCTTTGACCAACATATGACTAAGCCTTGAATGGTGGCTGTGACAGAAAGTAC	420
Qy	496	CATGTATGCGCACCAAACTGACACTACACAAAGAAAAGCTTAAAGACAAAGGAAACT	555
Db	421	CATGTATCAAAACCAAAAGCAAAACCTACAGAGAAAGGTGAAGATTTAGAGAGAGA	480
Qy	556	TACCGGCTCTAATACATGAACCTGATATGAAAGAGAGAAATCCGAATCAGGTTTTAAT	615
Db	481	CATGGAACCTCTTATGATGAATATATACAAACCTAGAGATCCACAGTATGGTTTTAGTG	540
Qy	616	GTTGAAAACCAAGTAGATTAATTATGAAATTCGATCCAAATGGAGTAGATGCTCCAG	675
Db	541	GACAAATGAAGCTGCTGTGGCACTTGCAATGGGGCTTCGAACCTCTATGCAATTCGGCTG	600
Qy	676	ATGTTTTCCTTAGGGTTGTTCATCCGAATCAGCCCAATCTGCTGTTAGGTTATGAA	735
Db	601	CATCAGGGCAACAACACCACACCATCTCCCTAATCTTACCTTGGAGATGATTTTGA	660
Qy	736	TGACATGATCTTAGCGCTGC	755
Db	661	GCCCATGAACCTTGCGCTTCC	680

```

RESULT 3
US-09-640-211A-10
: Sequence 10. Application US/09640211A
: Patent No. 6833446
: GENERAL INFORMATION:
: APPLICANT: Wood, Marion
: APPLICANT: Shenk, Michael A.
: APPLICANT: McGrath, Annette
: APPLICANT: Glenn, Matthew
: TITLE OF INVENTION: Composition and Methods for the
: FILE REFERENCE: 11000.1021C1U
: CURRENT APPLICATION NUMBER: US/09/640,211A
: NUMBER OF SEQ ID NOS: 2368
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 989
: TYPE: DNA
: ORGANISM: Eucalyptus grandis
US-09-640-211A-10

```

Query Match	23.6%	Score 216.6	DB 4	Length 989
Best Local Similarity	64.4%	Pred. 3.8e-49		
Matches 324	Conservative 0	Mismatches 179	Indels 0	Gaps 0
QY	73	GAGATGGGAGGGGGAAGATAGAGATATAAAAAGATAGAGAAATCCGACGAAACGCGAAGTT	132	
DB	4	GAGATGGGAGGGGGAAGATCCAGATCAAGCTGATAGAAACAGACGAAACGGCAGGTG	63	
QY	133	ACATATTTTAAAGAGAGAGTTGGGATCTGAAAGAGGCCAAGAGCTCATCTGTTCTCTGT	192	
DB	64	ACCTACTCGAAGCCACGAGAGCGGCTCTTCAAGAGAGCGAACGAGCTCACCGTCTTAGGC	123	
QY	193	GATGTCAGGCTGTCATCATATGTTCTCAAGCAGAGAAAGTGGCTGATTAATGCAGC	252	
DB	124	GACCCAGAGCTCATCATATATATCTCCAGCACCGGCAAGCTCCAGAGTATCATCAGC	183	

Db
483 CAAGAACAAATGCTGTTGAAGCTAACAGAGAAATTAAGGAAGAAGCTGGAAGAGA 538

RESULT 9

US-09-410-464-1
 Sequence 1, Application US/09410464
 Patent No. 6395892
 GENERAL INFORMATION:
 APPLICANT: Struense et al.
 TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 TITLE OF INVENTION: poplar and other plant species.
 FILE REFERENCE: 53375
 CURRENT APPLICATION NUMBER: US/09/410,464
 CURRENT FILING DATE: 1999-10-01
 EARLIER APPLICATION NUMBER: 09/287,700
 EARLIER FILING DATE: 1999-04-06
 EARLIER APPLICATION NUMBER: 60/080,851
 EARLIER FILING DATE: 1998-04-06
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 4285
 TYPE: DNA
 ORGANISM: *Populus balsamifera* subsp. *trichocarpa*
 US-09-410-464-1

Query Match	11.9%	Score 109.4	DB 3	Length 4285
Best Local Similarity	73.3%	Pred No. 1.6e-19		
Matches 140	Conservative	0	Mismatches 51	Indels 0
			Gaps	0

QY 70 AGAGACATGGGAGGGGGAAGTAGAGATAAAAAAGATAGAGAATCCGACGAACAGGCCAA 12

Db 1995 AAAAAATATGGGTCTGTGAAGAATTGAATCAAGAAGATCGAAAACCCCACAAACAGGC 20

0y 130 GTTCATATCTTAAGAGGAGAGTGGATCTGAAAGGCCAAAGAGCTCAGCTTC 189
 Db 2055 GTCACTACTCGAGGAGAGAAATGATTTTCAGAAAGCCCAAGAGCTCAGTACTT 2114

Db
07
190
2115

QY	250	AGCCCCCTCTAC	260
Db	2175	AGCCCCCTCCAC	2185

US-09-640
RESULT 10

```

; Sequence 2031, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Sheink, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2031
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2031

Query Match      11.9%; Score 109.2; DB 4; Length 412;
Best Local Similarity 74.2%; Pred. No. 5.6e-20;
Matches 138; Conservative 0; Mismatches 48; Indels 0; Gaps 0

```

Oy	70	AGGAGATGGGGGCGAAGAATAAGATTAAAAAAAGATAGAGATCCGACGACAGCAA	129
Dd	130	AGGAAGTGGCGAAAGAGATTAAGATTAAAGAGATGACCACTTGACGGCAGGCAG	189
Oy	130	GTTACTATTTCTAAGAGAGAGTGTGGATCTGAAGAAAGCCAAAGAGCTCATCTTTCTC	188
Dd	190	GTGACATTTCTCGAAGAGAGAGAAAGAGGGCTGATCAAGAAAGGCCGAGAGCTTCCTCGTCTG	249
Oy	190	TGTGAATGCTCAGGTCTCTCTCATCAATGTTCTCAAGCA CAGGAAAAGTTGGCTATTACTGC	248
Dd	250	TGTGAATGCTGAAGCTGTCTCTCATCGTCTTCTTAGCCACTGGCAAGCTCTATGATTTCTCC	308
Oy	250	AGCCCC 255 	
Dd	310	AGCTCC 315	

RESULT 11

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US-03-640-211A-97
; Sequence 97, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640, 211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: Faastsq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-97

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Query Match	11.5%	Score 105.8	DB 4	Length 396
Best Local Similarity	74.0%	Pred. No. 47e-19		
Matches 134, Conservative	0	Mismatches 47	Indels 0	Gaps 0

OY

71 GAGAGTGGCGAGGGAAGATAGAGTAATAAAAGAATAGAGATCCGCACCAAGCAG 13
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db

1 GAATAATGGGAGAGCGAAGATTGACTAAAGAGCATTTGAGATTGCAAATAGCAGGCCAG 60

[illegible]

Dy 191 GTGATCTAGGTCCTCTCATGTTCTCAAGCAGGAAGTGGCGATTACAC 23
| | | | | | | | | | | | | | | | | | | | |
Db 121 GTGATCTAGGTTGCTGTCAATCTTCCGATACTGGCAGCTTTACGAGTTCCA 18

QY	251 G 251
Db	181 G 181

RESOLV. 12
HIS-09-640

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: Sequence 1490: Application US/09640211A
: Patent No. 683346
: GENERAL INFORMATION:
: APPLICANT: Wood, Marion
: APPLICANT: Shenk, Michael A.
: APPLICANT: McGrath, Annette
: APPLICANT: Glenn, Matthew
: TITLE OF INVENTION: Modifications and Methods for the
: TITLE OF INVENTION: Modifications of Gene Transcription
: FILE REFERENCE: 11000.1021C1

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; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1490
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1490

Query Match 11.5%; Score 105.8; DB 4; Length 396;
Best Local Similarity 74.0%; Pred. No. 4,7e-19;
Matches 134; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 71 GAGAGATGGGAGGGGAGATAGATATAAAGATAGAGATCCAGACAGGCAAG 130
1 GAAAAATGGGAGAGGAGAAATGAGATTAAGAGATGAGATGCAATATGCGGAG 60

QY 131 TTACATATTCTAAGAGAGAGATTGGATCTGAAGAGCCCAAGAGCTCATCTCT 190
61 TTACATTTCTGAAAAGCCGTTCTGGTTGCTCAAGAGGCGAGAGCTCTCATCTCT 120

QY 191 GGTATGCTCAGGTCCTCTCATCATATGTTTCAGACAGAGAAAGTTGGTATTA 250
121 GTGATGCTGAGGTTGCTGTCTATATCTTCGAAATACGCGCAAGCTTTACAGTTCTCA 180

QY 251 G 251
DB 181 G 181

RESULT 13

US-09-640-211A-1952
; Sequence 1952, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1952
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1952

Query Match 11.2%; Score 102.8; DB 4; Length 475;
Best Local Similarity 68.1%; Pred. No. 3,4e-18;
Matches 143; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 46 GAAAAACGGGAGAAACAGGAGAGAGATGGGAGGAGGAGATAGATATAAAG 105
101 GCAAGCAAGTGAAGAGAGAGCAAAATATGCGAGAGAGAAATCAAGATCAGAG 160

QY 106 ATAGAGAAATCCGAGAGAGAGATTAATTTCTAAGAGAGAGATTGGATTA 165
161 ATAGACAAATGTGACGCGAGAGAGATGACGTTTCTAAGAGAGAGAGGCTTTTCAAG 220

QY 166 AAGGCCAAGAGAGCTCACTGTTCTGTGATGCTCAGGTTCTCTCATCATGTTTCAAGC 225
221 AAGGCCGAGAGAGCTGTGCTGCTGTGCGATGCCAGAGTCGCTGTCATTTCTCGGCT 280

QY 226 ACAGAGAAATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 255
281 ACCGCAAGCTTTTGTAGTACTCAAGCTCC 310
DB

RESULT 14
US-09-640-211A-69
; Sequence 69, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-69

Query Match 11.2%; Score 102.8; DB 4; Length 684;
Best Local Similarity 68.1%; Pred. No. 4,1e-18;
Matches 143; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 46 GAAAAACGGGAGAAACAGGAGAGAGATGGGAGGAGGAGATAGATATAAAG 105
310 GCAAGCAAGTGAAGAGAGAGCAAAATATGCGAGAGAGAAATCAAGATCAAGAG 369

QY 106 ATAGAGAAATCCGAGAGAGAGATTAATTTCTAAGAGAGAGATTGGATTA 165
370 ATAGACAAATGTGACGCGAGAGAGATGACGTTTCTAAGAGAGAGAGGCTTTTCAAG 429

QY 166 AAGGCCAAGAGAGCTCACTGTTCTGTGATGCTCAGGTTCTCTCATCATGTTTCAAGC 225
430 AAGCCGAGAGAGCTGTGCTGCTGTGCGATGCCAGAGTCGCTGTCATTTCTCGGCT 489

QY 226 ACAGAGAAATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 255
DB 490 ACCGCAAGCTTTTGTAGTACTCAAGCTCC 519

RESULT 15

US-09-640-211A-12
; Sequence 12, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-12

Query Match 11.1%; Score 102.2; DB 4; Length 342;
Best Local Similarity 71.7%; Pred. No. 4,2e-18;
Matches 134; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 68 AGAGAGATGGGAGGAGGAGAGATAGATATAAAGATAGAGATCCAGACAGAGC 127
1 AGAGATTAATGGGAGAGAGAGAGTGTGAGCTGAAAGAGATAGAGAAATCAAGATCAAGAGC 60
DB

Qy	128	AGGTTACATATCTTAAGAGAGAGTTGGATTA	CTGAAGAGCCCAAGAGCTCACTGTTG	187
Db	61	AGGTGACCTTCTCAAGAGAGAGATGGCTGTTGA	AGAGGCTATGAGCTCTGTGTC	120
Qy	188	TCTGTATGCTCAGCTCTCTCATCATGTTTCA	AGCAGAGAAAGTTGGCTGATTACT	247
Db	121	TGTGTATGTTGAGGTGCGCTCTCATCTTCTC	AGCGGTGCAAGCTCTATGAGTTTG	180
Qy	248	GCAAGCC	254	
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	316.8	34.5	980	20 US-10-690-246-3
5	245.2	26.7	637	21 US-10-487-901-7033
6	236	25.7	1257	21 US-10-343-477A-45
7	234.8	25.6	681	17 US-10-260-238-5530

8	228	24.9	946	14 US-10-104-580-2	Sequence 2, Appli
9	227.2	24.8	681	14 US-10-104-580-3	Sequence 3, Appli
10	216.6	23.6	989	20 US-10-856-499-10	Sequence 10, Appli
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13	209.8	22.9	664	21 US-10-487-901-3483	Sequence 3483, Ap
14	209.8	22.9	665	21 US-10-487-901-7018	Sequence 7018, Ap
15	207.2	22.6	926	21 US-10-343-477A-49	Sequence 49, Appl
16	203.4	22.2	630	21 US-10-487-901-7174	Sequence 7174, Ap
17	202	22.0	871	18 US-10-425-114-10670	Sequence 10670, A
18	201.2	21.9	498	11 US-09-732-627A-4479	Sequence 4479, Ap
19	198.4	21.6	1231	18 US-10-425-114-15025	Sequence 15025, A
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21	190.6	20.8	1212	18 US-10-425-114-11957	Sequence 11957, A
22	187.4	20.4	1155	18 US-10-424-599-66649	Sequence 66649, A
23	176	19.2	425	11 US-09-922-293-14	Sequence 14, Appl
24	170	18.5	432	11 US-09-922-293-16	Sequence 16, Appl
25	169.4	18.5	900	18 US-10-425-114-10295	Sequence 10295, A
26	169.4	18.5	933	18 US-10-424-599-33218	Sequence 33218, A
27	168.2	18.3	2237	18 US-10-425-114-13190	Sequence 13190, A
28	168	18.3	401	11 US-09-922-293-13	Sequence 13, Appl
29	167.4	18.3	2718	18 US-10-424-599-120795	Sequence 120795,
30	163.6	17.8	1007	18 US-10-425-114-14870	Sequence 14870, A
31	163.6	17.8	1021	18 US-10-424-599-65326	Sequence 65326, A
32	160.4	17.5	407	11 US-09-922-293-3394	Sequence 3294, Ap
33	159.6	17.4	964	20 US-10-739-930-33200	Sequence 3200, Ap
34	159.2	17.4	366	20 US-10-856-499-2008	Sequence 2008, Ap
35	155.2	16.9	360	11 US-09-922-293-15	Sequence 15, Appl
36	153.8	16.8	914	18 US-10-412-699B-55	Sequence 55, Appl
37	151.8	16.6	951	19 US-10-767-795-2121	Sequence 2121, Ap
38	151.2	16.5	896	15 US-10-278-536-238	Sequence 238, App
39	149.8	16.3	905	20 US-10-856-499-1944	Sequence 1944, Ap
40	148.6	16.2	474	11 US-09-732-627A-4667	Sequence 4667, Ap
41	148.2	16.0	639	19 US-10-021-323-8682	Sequence 8682, Ap
42	146.4	15.2	601	19 US-10-021-323-13542	Sequence 13542, A
43	145.6	15.9	742	21 US-10-487-901-3474	Sequence 3474, Ap
44	144.2	15.7	632	21 US-10-487-901-3376	Sequence 3376, Ap
45	143.4	15.6	409	20 US-10-856-499-1512	Sequence 1512, Ap

ALIGNMENTS

RESULT 1
US-10-690-246-1
: Sequence 1, Application US/10690246
: Publication No. US20040210967A1
: GENERAL INFORMATION:
: APPLICANT: CHEN, HONG-HUA
: TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
: FILE REFERENCE: U 014863-8
: CURRENT APPLICATION NUMBER: US/10/690,246
: PRIOR FILING DATE: 2003-10-21
: PRIOR APPLICATION NUMBER: 091125320
: PRIOR FILING DATE: 2002-10-25
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 1
: LENGTH: 917
: TYPE: DNA
: ORGANISM: Phalaenopsis equestris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (76)..(759)
US-10-690-246-1

Query Match 100.0%; Score 917; DB 20; Length 917;
Best Local Similarity 100.0%; Pred. No. 1e-231;
Matches 917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACGCGGATAGTAGAGGAAGAGGCGTTGAGACAGAAACAGCGGAGAA 60
|||||


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Db      1 ACCGGGATAGTAGAGAGAGAGAGAGAGGGTTGAGAACAGAGGAAAACAGGGAGAA 60
QY      61 CAGGGGAGAGAGAGATGGGAGGGGAGATGAGATTAATAAGATAGAAATCCGACG 120
Db      61 CAGGGGAGAGAGAGATGGGAGGGGAGATGAGATTAATAAGATAGAAATCCGACG 120
QY      121 AACGAGCAAGTTACATATTTAAAGAGAGATTGGGATACGTAAGAAAGCCAAAGAGCTC 180
Db      121 AACAGGCAATTTACATATTTAAAGAGAGATTGGGATACGTAAGAAAGCCAAAGAGCTC 180
QY      181 ACTGTTCTCTGTGATGCTCAGGTCCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCT 240
Db      181 ACTGTTCTCTGTGATGCTCAGGTCCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCT 240
QY      241 GATTACGACAGCCCTCTACTGATATTAAGGGGATATAGAGAGTCCAGGTTTGACT 300
Db      241 GATTACGACAGCCCTCTACTGATATTAAGGGGATATAGAGAGTCCAGGTTTGACT 300
QY      301 GGAATGATCTATGGAATGCTCAGTATAGAGAGATGAGAAATCGCTGAAGCATCTGAAT 360
Db      301 GGAATGATCTATGGAATGCTCAGTATAGAGAGATGAGAAATCGCTGAAGCATCTGAAT 360
QY      361 GAGATTACCAAAACCTGAGAGAGAGATTAAGAGAGAAAGGGGAGAAATTTGAGAGGC 420
Db      361 GAGATTACCAAAACCTGAGAGAGAGATTAAGAGAGAAAGGGGAGAAATTTGAGAGGC 420
QY      421 ATGGAATTAAGCAATCGCGGCTTGAAGCAATTTGGAAGAGTCTCTTGAATTTGT 480
Db      421 ATGGAATTAAGCAATCGCGGCTTGAAGCAATTTGGAAGAGTCTCTTGAATTTGT 480
QY      481 AGGATAGAAAGATATCATGTGATGCGCACAAACCTGACATTAACAAGAAAGCTTAA 540
Db      481 AGGATAGAAAGATATCATGTGATGCGCACAAACCTGACATTAACAAGAAAGCTTAA 540
QY      541 AGCAAGAGGAACTTACCGGCTCTTAATACATGATCGATATGAAAGAGAGAAATCCG 600
Db      541 AGCAAGAGGAACTTACCGGCTCTTAATACATGATCGATATGAAAGAGAGAAATCCG 600
QY      601 AACACGAGTTTAAATGAGAAACAGAGTAAATTTATGAAATTTGATTCAGATGCTG 660
Db      601 AACACGAGTTTAAATGAGAAACAGAGTAAATTTATGAAATTTGATTCAGATGCTG 660
QY      661 AATGAGTCTCAGATGTTTCTTTAGGTTGTTGATCCGATCAGCCCAATCTGCT 720
Db      661 AATGAGTCTCAGATGTTTCTTTAGGTTGTTGATCCGATCAGCCCAATCTGCT 720
QY      721 GGTTAGGTTATGATCAATGATCTTAGCCTTCATATGAGAGATTAATTAATTT 780
Db      721 GGTTAGGTTATGATCAATGATCTTAGCCTTCATATGAGAGATTAATTAATTT 780
QY      781 TATTGTTATTTTATTTATGTTTGAACCTTGAATTAAGAGAGGGGAGATCTATTGAGA 840
Db      781 TATTGTTATTTTATTTATGTTTGAACCTTGAATTAAGAGAGGGGAGATCTATTGAGA 840
QY      841 GAGAACTGCTTAAATTTGATTTCCGTTGTTCTCTTCATGTCAGTGAATTTT 900
Db      841 GAGAACTGCTTAAATTTGATTTCCGTTGTTCTCTTCATGTCAGTGAATTTT 900
QY      901 TTGTTTGTGTTTTCGG 917
Db      901 TTGTTTGTGTTTTCGG 917

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RESULT 2
US-10-690-246-7
; Sequence 7, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, MEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246

```

```

; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)..(782)
US-10-690-246-7

```

```

Query Match      39.0%; Score 357.6; DB 20; Length 898;
Best Local Similarity 75.7%; Pred. No. 8.5e-84;
Matches 457; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

```

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QY      76 ATGGGAGGGGAGAGATAGAGATTAATAAGATTAAGAAATCCGACGACGAGGATTACA 135
Db      123 ATGGGAGAGGAGAGATAGAGATTAATAAGATTAAGAAATCCGACGAGGATTACA 182
QY      136 TATTCTAAGAGAGAGTTGGGATCTGAAAGAGGCCAAGGAGCTCACTGTTCTGTGAT 195
Db      183 TATTCAAAAGAGGAGCTTGGGATCATGAAGAGGAGAGAGAGCTCACTGTTCTGTGAT 242
QY      196 GCTCAGGTCCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGACGCCCC 255
Db      243 GCTCAAGCTCTCATCATCTCTTCAAGCTCGGGAAGTTAGGATTTCTGACGCCCC 302
QY      256 TCTACTGATTTAAGGGGATATATGAGAGGTAACAGGTTGATCTGAAATGATCTATGG 315
Db      303 TCCACAGAGGTTAAGATATATGTTGAGAGGTAACAAAGTTTACCGGAATGATATATGG 362
QY      316 AATGCTCAATTAAGAGAGATGAGAAATAGCGTGAAGCATCTGAATGAGATTAACCAAAAC 375
Db      363 GATGCGCAATATCAAGAGATGAGAAACCTTGAAGAAATCTCAAGGAGTTAATGTTAAT 422
QY      376 CTGAGAGAGAGATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
Db      423 CTTCAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
QY      436 CTGCGGGCTCTTGAAGCAATTTGGAAGAGTCTTTGAATTTGTTAGGCAATGAAGATAT 495
Db      483 CTGCGGGCTCTTGAAGCAATTTGGAAGAGTCTTTGAATTTGTTAGGCAATGAAGATAT 542
QY      496 CATGTATGCGCCACAAACCTGACACTTCAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 555
Db      543 CATGTATGCGCTTACGCAACAGACCTTGCAGAGAAAGAGAGAGAGAGAGAGAGAGAG 602
QY      556 TACCGGCTCTTAATATCATGAATCTGATA--TGAAAGAGAGAGATCCGAATCAAGGTTT 612
Db      603 TACAGAGCCCTTACGATGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
QY      613 AATGTAAGAAACAGAGATGAATTTATGAATTTGATTCATGATGATGATGATGATGAT 672
Db      663 CTGTAAGAGATTAAGTGAATCTATGACAGCTCAATCTCAATGCAATGCAATGCAATG 722
QY      673 CAGA 676
Db      723 CGGA 726

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RESULT 3
US-10-690-246-5
; Sequence 5, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, MEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246

```

US-10-690-246-5

Query Match	35.4%	Score 324.2;	DB 20;	Length 1036;
Best Local Similarity	69.1%;	Pred. No. 6.3e-75;		
Matches 475; Conservative	0;	Mismatches 203;	Indels 9;	Gaps 2;

OY	7	AGATGGGAGGGGGGAATGAGATTAATAAAGATGAGATCCGACGAACGGCAAGTTA	13
Db	214	AGATGGGAGGGGGGAATGAGATTAATAAAGATGAGATCCGACTAATCGGCGAGGTGA	272
OY	134	CATATTTCTAAGAGAGAGTTGGGATCTGAAGAGGCCCAAGAGCTCATCTGTCTCTGTG	193
Db	274	CTTACTCGAAGAGAGAGAGCTGGGATTTATAGAAAGGCGAGGAGATCACTGTCTCTGGG	333
OY	194	ATGCTGAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAGTTGGCTGATTACTGCAAGC	253
Db	334	ATGCTGAGGTTTGGCTTATCATGTTCTCGAGATCTGGAAAGTTTCTGAGATCTGTAGCC	393
OY	254	CTCTCACTGATATTTAAGGGGATATATAGAGGTAACGAGTTGTGACTGGAATGCATCTAT	313
Db	394	CTTCGACGGAAGAGAAAGTTTGTGAACGCTACACAGAGGTATCTGGCATTTACTGT	453
OY	314	GGATGCTCATGTATGAGAGATGCAAAATACGTGAAGACTGATGATGATTAACAA	373
Db	454	GGAGCTCGAGTACGAGAGATCTGAATACCTTAACATTCGAAGAGATCAATCCGA	513
OY	374	ACCTGAGAGAGAGATTGAGAGAGAGAGAGAAATYGAGGGCATGACATTAAGC	433
Db	514	ATCTGAGAGAGGAAGTATAGGCACAGAGATGGGGAGATCTTGAGGGACTGATATCAAGG	573
OY	434	AACTCGCGGCTTTGAGCAAACTTTGGAGAAGTCTTTGAATTTGTAGGCTATAAAGT	493
Db	574	AACTCGCGGCTTTGAGCAAAACATTTGATGAGGCAATGAGCTAATGCAAAATTAAGAAAT	633
OY	494	ATCATGTGATCGCACAAACTGACACTTACAAAGAAAGCTTTAAAGCACAAGGAAA	553
Db	634	ATCATGTGATGAGTCTCAACCGGACACTTACAAAGAAAGTTGAAAGACTCCCAAGAAA	693
OY	554	CTTACCGCGCTTATATCATGAATCGATATGAAAGAGAGAGATCCGAATACGAGTTTAA	613
Db	694	CACACCGGAACCTTAATGCAAGAAATGGAAATCGTTGAGGACCAACCAAGTATGAGTTCC	753
OY	614	ATGTGAGAAACCGAGAGTGAATTAATCAAAATTCGATTCGATGAGATGATGATGCTCC	673
Db	754	ACG-----AGATTCAAGCAATTAAGAGGGGTCTTGCTCTTGGAAATGACGGGCTTC	803
OY	674	AGATGTTTTCTTTAGGGTTGTTCATCCGATCAGCCCAATCTGCTTGGTTTAAAGTTATG	733
Db	808	ACATGTTATGCTTCGG--GTGCAACCAACCAAAATCTTACAGGAACGGGATATA	863
OY	734	AATCAATGATCTTAAGCTTGCAATAT	760
Db	865	GCTCTCAAGATCTTGCGCTGCTGAT	891

RESULT 4
US-10-690-246-3
; Sequence 3, Application US/10690246
; Publication No. US20040210367A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA

```

? APPLICANT: TSAI, MEN-CHIEH
? TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
? FILE REFERENCE: U 014863-8
? CURRENT APPLICATION NUMBER: US/10/690,246
? CURRENT FILING DATE: 2003-10-21
? PRIOR APPLICATION NUMBER: 091125320
? PRIOR FILING DATE: 2002-10-25
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 3
? LENGTH: 980
? TYPE: DNA
? ORGANISM: Phalaenopsis equestris
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (196) .. (864)
US-10-690-246-3

34.5%; Score 316.8; DB 20; Length 980;
Best Local Similarity 65.3%; Pred. No. 5.5e-73;
Matches 503; Conservative 0; Mismatches 252; Indels 15; Gaps 2;

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US-10-690-246-3

Query Match	34.5%	Score 316.8	DB 20	Length 980
Best Local Similarity	65.3%	Pred. No. 5.5e-73		
Matches 503	Conservative 0	Mismatches 252	Indels 15	Gaps 2
QY	65	GGAAGAGAGAGATGGGGGAGATAGAGATAAAAAGATAGAGATCCGACGAACA	124	
DB	185	GAAAGAGAACATGGGGGAGGAGATCGAGATAAAGATGAGAACCTCCACAAACA	244	
QY	125	GGCAAGTTACATATTTCTAAGAGAGAGTTGGGATATCGAAGAAAGCCAGGAGCTACTG	184	
DB	245	GGCAGTTACTTACTCTAAGAGAGAGGCTGGGATCATGAAAAAGCCGACGAGCTCACGG	304	
QY	185	TTCTCTGATGATCTCAGGTCCTCTCATCATGTTCTCAAGACACAGAAAGTTGGCTGATT	244	
DB	305	TTCTCTGATGATCTCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	364	
QY	245	ACTGACGCCCTCTACTGATATTAAGGGGATATATGAGGATACAGGTTGACTGCA	304	
DB	365	ATTGATGCTTACACACCGATACCAAGATGATATGATCTTTACACAGAGGTGTCGGCA	424	
QY	305	TGATCTATGGAATGCTCAGATATAGAGAGATGCGAATAGCTGAGCATCTGAATGAGA	364	
DB	425	TAAATTTATGAGAGCAGAGATACGAGAAAGATGCAATACCTTGATATATTTGAGAGGA	484	
QY	365	TTAACCAAAACCTGAGAGAGAGATTAGAGAGAGAAAGGGGAGAAATYGAGGGCATGG	424	
DB	485	TAAACCAACAATTGAGAGAGAGATTAAGCAGAGAGATGGGGAGAGATTTGAAGGGCTAG	544	
QY	425	ACATTAAGCAACTGCGCGGCTTTGAGCAAACTTTGGAAGAGTCTTTGAATTTGTAGGC	484	
DB	545	AAATCAAGAACTGGTGGTCTTGAGCAAAATATGACAGAGGCCCTTAAGCTGTATAGGA	604	
QY	485	ATAGAAATATCATATGATTCGCCACACAACTGACACTTAAGAAGAAAGCTTAAGACA	544	
DB	605	ATCGAAATATCATCTCATACAGCACCCACAGACATTCACAAAAGAAAGTTGAAGAACT	664	
QY	545	CAAGGAAACTTACCGCGCTCTAATACATGAACTGATATGAGAAAGAGAGATCCGAACT	604	
DB	665	CTCAAGAAACCAAGAACTTACCTCGGAGGCT-----GGAACCTGAGCACG	712	
QY	605	ACGGTTTAAATGTAGAAAACAGAGATAGATTTATGAAATTCATTTCCATATGTGATG	664	
DB	713	CCGTCTACTACGTGATGATGATTCMAACAATAAGATGAGCGCGCTTSCACTTGGAATG	772	
QY	665	AGTGCCTCAGATGTTTCTTTAGGGTGTGTCATCCGATACAGCCCATCTTGTT	724	
DB	773	GGGCTTCTCATCTGATTCATTTGCG---TACCAACCAAGCAGCGAAGCTTGAGGGAG	829	
QY	725	TAGGTATGAATCACATATCTTAGCCTTGACATTAATGACAGTAAATTAATGATTTTAT	784	
DB	830	TTGATATATGCTCATGATCTACGCTTCGCTGATCTTTATATATTCGATGCGCAACTG	889	
QY	785	GATTTTTATTTATGTTTGAACCTTATGAATATATGAGATGGGGATCTA	834	
DB	890	CTTAATATATCTATGATCTGATGTCTTACGCTTCAAGATAGGGGTCTA	939	

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RESULT 5
US-10-487-901-7033
; Sequence 7033, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddaeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avuln
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7033
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7033

```

Query Match	26. 7%;	Score 245.2;	DB 21;	Length 637;
Beet Local Similarity	71.0%;	Pred. No.3.8e-51;		
Matches 325;	Conservative 0;	Mismatches 133;	Indels 0;	Gaps 0
QY	76	ATGGGAGAGGGGAGATAGATGATTAATAAAGATAGAGAAATCCGACGAAACAGGCAAGTTACA	135	
Db	180	ATGGGGAAGGGCGAAGTCAGATCGAAGCGGATCGAGAACGCCACCAACAGGCAAGTTGACC	239	
QY	136	TATTTAAGAGAGAGATTGGGATCTGAAGAAAGCCAGAGACTCACTGTTCTTGTAAT	195	
Db	240	TACTCGAAGCGCCGACGGGGATCATGAAAGAAAGCCAGGGAACCTACCGTGCTTCGCGAC	299	
QY	136	GCTCAGAGTCTCTCATCATGTTCTTCCAACGACACAGGAAATGGTGGCTGATCTACGACGCC	255	
Db	300	GCCCAAGTTCGCATCATGTTCTCTCCACCGGCAATACACAGATTTCTCGACCCCT	359	
QY	256	TCTACTGATATTAAAGGGGATATATGAGAGATCACGGTGTGACTGGAATGAGATCTATGG	315	
Db	360	TCCACGACATCAAGGGGATCTTTGACGGCTACAGCAAGCCATGGGACACAGCCTTTGG	419	
QY	316	AATGCTCAGTATGAGAGATGCGAATACGCTGAGACATCTGATATGATTAACCAAAAC	375	
Db	420	ATCGAGCACTATGAGAAATGTGACGCGCAGCTGAGGCACTTCAAGGACATCAACCGCAAC	479	
QY	376	CTGAGGAGAGAGATTAGAGAGAGAAAGGGGAGGAATTGAGGGCATGGAATTAAGCAA	435	
Db	480	CTGCGCACCGAGATCAGGCAAAAGATGGGAGAAAGATCTGACGGGCTTGAGTTCCGACGAG	539	
QY	436	CTGCGCGGTCCTTGAGCAAACTTTGGAAGAGTCTCTTAGAATTTGTTAGGATGAAGATAT	495	
Db	540	CTGGCGGGCTTGAGGAAATGTGATGCGCGGCTCAAGAGAGGTTGGCACAAGAAATAT	599	
QY	496	CATGTGATGCCACACAAACTGACACTTTCAGAAAAA	533	
Db	600	CATGTGATCAGACACAGACTGAACCTTCAAGAAAAA	637	

RESULT 6

US-10-343-477A-45

; Sequence 45, Application US/10343477A

; Publication No. US20050066394A1

```

; GENERAL INFORMATION:
; APPLICANT: Olga Danillevskaya
; APPLICANT: Pedro Hermon
; APPLICANT: Ed Bruggemann
; APPLICANT: David Shitbroun
; APPLICANT: Evgenii Ananiev
; APPLICANT: J. Antoni Rafalecki
; APPLICANT: Hajime Sakai
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Rebecca R. Cahoon
; APPLICANT: Theodore M. Klein
; TITLE OF INVENTION: Floral Development Genes
; FILE REFERENCE: DD0014-PCT-USR
; CURRENT APPLICATION NUMBER: US/10/343,477A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/253,415
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US01/43750
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-343-477A-45

```

Query Match	25.7%	Score 236	DB 21	Length 1257
Best Local Similarity	59.1%	Pred. No. 1.5e-51		
Matches 404	Conservative 0	Mismatch 280	Indels 0	Gaps 0
Qy 75	GATGGGAGGGGGGAAGTAGATGATAAAAAAGATAGAAATCCGACGAAACAGCGCAAGTTAC	134		
Db 130	GATGGGGCGCGCGCAAGATCCAGATCAAGCGGATGAGAAAGCCACCAACCGCCAGGTGAC	189		
Qy 135	ATATTCTAAGAGAGAGTGGATCTGAAGAGGCCAAGAGCTCATCTGTTCTCTGTGA	194		
Db 190	CTACTCCAAAGCGCGGAGGATCAAGAAAGGCGCGAGCTCAACCGTCTCTCCGA	249		
Qy 195	TGCTCAGGTCCTCTCATATGTTCTCGAAGACAGAAAGTTGGCTGATTAAGTCAAGCCC	254		
Db 250	CGCCAGGTCGCATCATGTTCTCTCCACCGGAAAGTACAGAGATTTCTGACGCC	309		
Qy 255	CTTACTAGATTTTAAGGGGATAATATGAGAGTACAGATTGTGACTGGAATGATCTATG	314		
Db 310	CGGAACGACATCAAGACATCTTTGACCGGTACACAGCGCATGGGACCAAGCTATG	369		
Qy 315	GAATGCTCAGTATGAGAGATGCAGAAATCGCTGAAGCATCTGAATAGATTAACAAA	374		
Db 370	GATGAGAGATATGAGAAATATGACGCCACGCTGAGCATCTCAAGACATCAATCTGTG	429		
Qy 375	CCTGAGGAAGAGATTATGAGAGAGAAAGGGAGAGAAATTTGAGGGCANTGACATAAAGCA	434		
Db 430	TCTGGGCAAGAGATTAGGCMAAAGAGATGGGAGAGATCTGGACGTCTGGACTTGCAGCA	489		
Qy 435	ACTGGCGCGTCTTAGGCMAAATTGGAAGAGTCTCTTAGAATTTGTAGGCAATAGAAATGA	494		
Db 490	GCTGGCGGCGCTCGAGCMAACGTTCGACGCGGCTCTCAAGAGAGTTGGCCATAGAAATGA	549		
Qy 495	TCATGTGATCGCCACACAACTGACACTTACAAAGAAAAGCTTAATAAAGCACAAAGGAAAC	554		
Db 550	CCATGTGATGACGACGCACTGATTAACCTACMAAAGAAAGGTGAAGCACTGCACGAGGC	609		
Qy 555	TTACCGCGCTTAATACATGAATCTGGAATATGAAGAAGAGAAATCCGAATCAGCGTTTAA	614		
Db 610	GTACAAAGAACTTGACGAGCGAGCTAAGCAATCCGAGAGACCCGCGTTCGGGTACGTGA	669		
Qy 615	TGTAGAAAACAGAGTAGAATTTATGAATAATTCATTTCAATGCTGATGATGATCTCTCA	674		
Db 670	CAACACGGGCGCGCGCTGCGCTGGAGACGGCGCGCGCGCGCTGTGGCGCGCGCGCGCC	729		
Qy 675	GATGTTTTCTTTAGGGTTGTTCATCCGAATCAGCCCAATCTGCTGGTTTAAAGTTATGA	734		

Db 730 GGAATGATACGCTTCCGCGTGTGCCCAAGCCCAACCTGACAGGCAATGCGCTAAG 789
QY 735 ATCAATGATCTTAAAGCTTGCATTA 758
Db 790 CTTCAAGACCTCGCGCTGGGCTTA 813

RESULT 7
US-10-260-238-5530

; Sequence 5530, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreppe, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 5530
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-260-238-5530

Query Match 25.6%; Score 234.8; DB 17; Length 681;
Best Local Similarity 65.8%; Pred. No. 2.2e-51;
Matches 341; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATATAAAGATAGAGATCCGAGAACGCAAGTAA 135
Db 1 ATGGGAGGGGGAAGATAGATATAAAGATAGAGATCCGAGAACGCAAGTAA 60
QY 136 TATTTAAAGAGAGATTGGGATATCTGAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
Db 61 TACTCAAGCCCGGACGGGATCATGAAAGAGCGCGGAGCTCACCGTCTCTGCGAC 120
QY 196 GCTCAGGCTCTCTCATATGATGTTCTCAAGCAAGGAAGTTGGCTGATTAATGAGCCCC 255
Db 121 GCCCAGGTGCGCATCATATATGTTCTCTCCACCGGCAAGTACACAGATTTGAGGCC 180
QY 256 TCTACTGATTTAAGGGGATATATGAGAGTACAGAGTTGATGTAAGTGAATGATATG 315
Db 181 GGAACCGATCAAGACATCTTTTACCGGATCCAGAGGCAATGAGGACCAAGCTTAAG 240
QY 316 AATGCTCAGTATGAGAGATGCAAGATACGCTGAAGCATCTGAATGAGATTAAACCAAC 375
Db 241 ATCGAGCATATGAGATATGCAAGCGCAAGCTGAGCCATCTCAAGAGATCATATGTG 300
QY 376 CTGAGGAAGAGATTAG 435
Db 301 CTGCGCACAGAGATTAG 360
QY 436 CTGCGCGGCTTTGAGCAAACTTTGAGAGAGTCTTTAGAAATGTTAGAGATGAAGTAT 495
Db 361 CTGCGCGGCTTTGAGCAAACTTTGAGAGAGTCTTTAGAGAGTTCGCAATAGAGATAC 420
QY 496 CATGTGATGCGCACAAACTGACACTTAAGAAAGAAAGCTTTAAAGACCAAGGAAACT 555

Db 421 CATGTGATGAGACCGAGACTGATACCTAAGAAAGAAAGTGAACACTCGGACGAGGCG 480
QY 556 TACCGCGCTTAAATACATGAATGATGATGATGATGATGATGATGATGATGATGAT 593
Db 481 TACAAAGAACTGACAGAGAGAGCTTAGCATGCGGAGAGA 518

RESULT 8
US-10-104-580-2

; Sequence 2, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (1) .. (684)
US-10-104-580-2

Query Match 24.9%; Score 228; DB 14; Length 946;
Best Local Similarity 58.3%; Pred. No. 1.6e-49;
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATATAAAGATAGAGATCCGAGAACGCAAGTAA 135
Db 1 ATGGGAGGGGGAAGATAGATATAAAGATAGAGATCCGAGAACGCAAGTAA 60
QY 136 TATTTAAAGAGAGATTGGGATATCTGAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
Db 61 TACTCAAGAGAGAAATGATATTTCTCAAGAGCCCAAGAGCTCACTGATTTGTGAT 120
QY 196 GCTCAGGCTCTCTCATATGATGTTCTCAAGCAAGGAAGTTGGCTGATTAATGAGCCCC 255
Db 121 GCTAAGTCTCTTTATCATATGTTCTCTCAACATTAACAACTCAATGATTAAGCCCC 180
QY 256 TCTACTGATTTAAGGGGATATATGAGAGTACAGAGTTGACTGGAATGATCTATG 315
Db 181 TCCATATCGACAAAGAGATCTAGATCAATATCAAGAACCTTTAGGATAGATCTGTG 240
QY 316 AATGCTCAGTATGAGAGATGCAAGATACGCTGAAGCATCTGAATGAGATTAAACCAAC 375
Db 241 GGCACCTAATACAGAGAAATGCAAGACACTTGAAGAGTGAATGATATCAATCATAG 300
QY 376 CTGAGGAAGAGATTAG 435
Db 301 CTGAGCAAGAGAAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 436 CTGCGCGGCTTTGAGCAAACTTTGAGAGAGTCTTTAGAAATGTTAGAGCATAGAAAT 495
Db 361 CTGCGCGGCTTTGAGCAAACTTTGAGAGAGTCTTTAGAGAGTTCGCAATAGAGATAC 420
QY 496 CATGTGATGCGCACAAACTGACACTTAAGAAAGAAAGCTTTAAAGACCAAGGAAACT 555
Db 421 CATGTGATCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 480
QY 556 TACCGCGCTTAAATACATGAATGATGATGATGATGATGATGATGATGATGAT 615

Db 481 CATGAAACCTCTTGATGGAATATGAAAGCAAACTAGAGATGACGATATGGTTAGTG 540
Qy 616 GTTGAAAAACCAAGTAGAATTTATGAAAATTCGATTCCATGGAATGATGTCTCCAG 675
Db 541 GACAAATGAACTGCTGTGTGCACTTGGCAATGAGGGCTTCCAACTCTATGATCCGCTG 600
Qy 676 ATGTTTCTTTAGGGGTGTTCATCCGAATCAGCCCAATGCTGTGGTTAGGTTATGA 735
Db 601 CATCAGGGGCAACACCAACCATCTCCCTAATCTTCACTTGAGATGATTTGGA 660
Qy 736 TCACATGATCTTAGCCCTTGCAATTA 759
Db 661 GCCCATGAACCTTGCCCTTGA 684

RESULT 9
US-10-104-580-3
; Sequence 3, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; TITLE OF INVENTION: Poplar and other plant species.
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-10-104-580-3

Query Match 24.8%; Score 227.2; DB 14; Length 681;
Best Local Similarity 58.4%; Pred. No. 2.2e-49;
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

Qy 76 ATGGGAGGGGGAAGATAGAGATTAATAAGATAGAGAAATCCGACGACAGGCAAGTTACA 135
Db 1 ATGGGAGGGGGAAGATTTGAATCAAGAAATGCAAAACCCCAAAACAGGCAAGTACC 60
Qy 136 TATTCTAAGAGAGAGTTGGATTACTGAAGAGCCAAAGAGCTCACTGTTCTCTGTGAT 195
Db 61 TACTCGAAGAGAAATGATATTTCAGAAAGCCCAAGAACTCACTGATCTTGTGAT 120
Qy 196 GCTCAGGTCTCTCATCATGTTTCTCAAGCAGAAAGTTGGTGTATCTGAGCCCC 255
Db 121 GCTAAGGTCTCTTATCATGTTTCTCCAACTGAACCACTGAATGATCATTAAGCCC 180
Qy 256 TCTACTGATATTAAAGGGATATATAGAGGTAACAGGTTGTGACTGGAATGATCTTAAG 315
Db 181 TCCCATGACAAAGAAATGATCAATATATAGAAAGCTTTAGGCAATGATCTGTGG 240
Qy 316 AATGCTCAGATAGAGAGATGACAGAAATACGCTGAAGCATCTGAATGAATTAACCAAAC 375
Db 241 GGCACTCAATACGAGAAATGCAAGAGCACTTGAGAAAGCTGAATGATTAATCAATCAATAG 300
Qy 376 CTGAGGAAGAGATTAGAGAGAGAGAGGGGAGAAATTGAGGGCATGACATTAAGCAA 435
Db 301 CTGAGCAAGAAATCAGAGCAGAGAGAGAGGGGCTTGATGATCTGAGCATTTGATCAT 360
Qy 436 CTGGCGGCTCTTGAAGCAAACTTTGAGAAAGTCTTTGAATTTGTTAGGCAATAGAAAGTAT 495

Db 361 CTGGCGGCTCTTGAAGCAATATGACTGAAGCCTTGAATGTTGTGCTGTGGCAGAAATGAC 420
Qy 496 CATGTATGTCCACACAACTGACATCTTACAGAAAAAGCTTAATAAGCAAGGAAACT 555
Db 421 CATGTATGTAAACAAACAAACCAAACTACAGAAAGAGTAAAGAAATTAAGAGAGACA 480
Qy 556 TACCGGCTCTTAATACATGAATGATATGAAGAGAGAAATCCGAATCAAGCTTTTAAT 615
Db 481 CATGAAACCTCTTGAATGAAATATGAAAGCAAACTAGAGATCGACAGTATGTTAGTG 540
Qy 616 TAGAAAACCAAGTAGAATTTATGAAAATTTGATTCGAATGATGATGTCCTCAG 675
Db 541 GACAAATGAAAGCTGTGTGCACTTGCAAAATGGGGCTTCCAACTCTATGATTCGCTG 600
Qy 676 ATGTTTCTTTAGGGGTGTTCATCCGAATCAGCCCAATCTGCTTGTGTTAGTTATGA 735
Db 601 CATCAGGGGCAACACCAACCATCTCCCTAATCTTCACTTGAGATGATTTGGA 660
Qy 736 TCACATGATCTTAGCCCTTGC 755
Db 661 GCCCATGAACCTTGCCCTTCC 680

RESULT 10
US-10-856-499-10
; Sequence 10, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-10

Query Match 23.6%; Score 216.6; DB 20; Length 989;
Best Local Similarity 64.4%; Pred. No. 1.7e-46;
Matches 324; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 73 GAGATGGGAGGGGGAAGATAGAGATTAATAAGATAGAGAAATCCGACGACAGGCAAGTT 132
Db 4 GAGATGGGAGGGGGAAGATCCAGATCAAGCTGATAGAAACACGACGAAACGGCAGTG 63
Qy 133 ACATATTTCTAAGAGAGAGTTGGATCTGAAGAGCCCAAGAGCTCACTGTTCTGTG 192
Db 64 ACTTACTCGAAGAGAGAGAAACGGGCTTTCAAGAGCCAAAGAGTCAACGCTCTAGGC 123
Qy 193 GATGTCAGGTCCTCTCATCATGTTTCTCAAGCAGAAAGTTGGCTGATTACTGACG 252
Db 124 GACCCCAAGGTCTCATCATGATCTCCAGACCGGCAAGCTCCACAGTACATCAAC 183
Qy 253 CCTCTACTGATATTAAAGGGATATATGAGAGTACCAAGTTGTGACTGAAATGATCTTA 312
Db 184 CCTTCACTCAACGAAAGAGTATGATCATGATATCAACAGGCTTCAGGTTGATCTC 243
Qy 313 TGAATGCTCAGATAGAGAGATGACAGATTAAGCTGAAACATCTGATAGATTAACCAA 372
Db 244 TGAAGCTTCACTATAGAAAGATGCAAGAACTGAGAAAGCTGAGAGAGGTGAACAAG 303
Qy 373 AACCTGAGAGAGATTTAGAGAGAGAAAGGGGAGAAATTGAGGCGCATGACATTAAG 432
Db 304 AACCTTCACTGAGAGGTCAAGAGAGGTTCCGGGAAAGACTGAATGTTAGCTTATG 363

OY 433 CAATCGCGGCTTGGACAACTTGGAAAGTCTTTAGATTGTTAGCCATAGAAAG 492
DB 364 GAATTGGCGGCTTGGACAAAGATATGCAAGCCCTTATCCCTGAAACCGAAG 423
OY 493 TATCATGTATGCGCCACAACTGACATTACAGAAAAAGCTTAAGCACAGGAA 552
DB 424 TACAGACGCTCGGCATCAATTCGACCGCCGAGAAAGAAAAAGATTGCTGAGAA 483
OY 553 ACTTACCGCGCTCTAATACATGA 575
DB 484 ATAAACAAAGTCTCTCGAAGA 506

RESULT 11

US-10-021-323-8631
; Sequence 8631, Application US/10021323
; Publication No. US2004012334A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, J11
; APPLICANT: Peng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8631
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(644)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-013-Q1-K6-F12
US-10-021-323-8631

Query Match 23.4%; Score 215; DB 19; Length 644;
Best Local Similarity 62.1%; Pred. No. 3.7e-46;
Matches 338; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

OY 56 GAGAACAGGGAAGAGAGATGGGAGGGGAGATGAGATAAAGATAGAGATC 115
DB 12 GAAAACTAGATTAAATTAATATGCTCGAGGAAAGATCAAGTCAAGTATAGAACT 71
OY 116 CGAACAAGGCAAGTATATTTCTAAGAGAGATTGGATATCTGAAAGGCCAAG 175
DB 72 CGACCAAGGCAAGTCACTATTCGAAAGAGAAACCGCTTTTCAAGAAAGTATG 131
OY 176 AGCTCACTGTTCTCTGATGCTCAGTCTCTTCATCATGTTTCAAGCAAGAAAGT 235
DB 132 AACTTACAGTTCTTGGCATGCTAGAGTTTGCATCATATGTTTCCACTGCTAAGC 191
OY 236 TGGCTGATTACGACCCCTCTACTATTTAAGGGGATATATGAGAGTTACAGGTTG 295
DB 192 TCCATGATTTATCGCCCTTCCACACAGAGCAAGTAATGATCAAGTACAGAAAA 251
OY 296 TGACTGATGATCTATGATATGCTCAGTATGAGAGATCAGAAATACGCTGAAGCATC 355
DB 252 CTTGGGATGATATCTGAAACACCACTATGAGAAATGCAAGAGCAAGTTGAAGCAGC 311
OY 356 TGAATGATTAACCAAACTGAGAAAGAGATTAGAGAGAGAGGGGAGGAATTGG 415
DB 312 TGAAGAGATTAAACGAACCTGCGCAAGATTAGAGAGATGGGCGACTGTTTGA 371
OY 416 AGGGATGAGCATTAAGCACTGGCGGCTTGAAGCAACTTTGGAAGGCTCTTTAGAA 475
DB 372 ATGATTTAGCATCAAGATCTTGTGCTTTGAAACAAAGAAATGAGAGCTCTGTCACTC 431

OY 476 TTGTTAGCATGAAAGTATCATGTGATGCCACAACTGACACTTACAGAAAAAGC 535
DB 432 TTAATTCGATGAAAGATCGTGTCTCTCAACCAAGATTCGATCTTCAAGAAAAAG 491
OY 536 TTAAGACCAAGGAACTTACCGGCTCTAATACATGAACTGATATGAAAGAGAGA 595
DB 492 TAGGAATGTGAAGAGATACCAAAATCTTTATCATGAACTGGAATCCCTGAAGAAAG 551
OY 596 ATCC 599
DB 552 ATCC 555

RESULT 12

US-10-424-599-120794
; Sequence 120794, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120794
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1
US-10-424-599-120794

Query Match 22.9%; Score 210.4; DB 18; Length 1036;
Best Local Similarity 62.6%; Pred. No. 7.8e-45;
Matches 328; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

OY 76 ATGGGAGGGGGAAGATAGATAAAGATAGAGATCCGACGAACAGGCAAGTTACA 135
DB 27 ATGGCTCGAGAAAGATCCGATCAAGAGATAGAGAAKCAACCAACCCCGAGTACT 86
OY 136 TATTTAAGAGAGAGTTGGATATCTGAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
DB 87 TATTTAAGAGAGATGCGCTTTTCAAGAGCCCAAGCTCACCGTTTATATGCGAT 146
OY 196 GCTCAGTCTCTCATCATGTTTCTCAAGCAAGAAAGTTGGCTGATTTACGAGCCC 255
DB 147 GCCAAGGTTTCTATATATATGTTCTCCAGCATGGGAAATCCACAGTACATCAATC 206
OY 256 TCTACTGATATTAAGGGGATATATAGAGGATACCAAGGTTGACTGAAATGATCTATG 315
DB 207 TCACTCAACAAAGCACTTCTTCAATCAATGACTGAGAGTCAATCTG 266
OY 316 AATGCTGATGAGAGATGAGAAATACGCTGAAGCATGAAATGATTAACCAAAAC 375
DB 267 AACTCTATTAAGAGATATGCAAGAGACTGAAAGAACTGAAGAAATGGAATAGGAAT 326
OY 376 CTGAGAAAGAGATTAGAGAGAGAGAGGAGAAATTGAGAGGCATGACATTAAGCA 435
DB 327 CTTGTAAGAGATTAGAGAGAGATGGAGATTGTCTGAACGATCTGGGCAATGGAAT 386
OY 436 CTGCGGCGTCTTGAAGCACTTGAAGAGTCTTTGAATGTTTGAAGCATATGAAGTAT 495
DB 387 CTCAAGCTCTTGAAGAGAAATGACAAAGCCCGCAAGTTGTTGAGCGTAATGAT 446
OY 496 CATGTATGCGCACAACTGACACTTACAGAAAAAGCTTAAGCAACAGGAAACT 555
DB 447 AAGGTATTAACAATATGATTAAGACCAAGAGGAAAAAGTTATATACGAGAAAGAGTG 506

Qy 556 TACCGGCTCTAATACATGAGTGAATGAAAGAGAAATCC 599
Db 507 CACAAACAGACTCTGTCATGACTTGATGCAAAAGCAGAAATCC 550

RESULT 13

US-10-487-901-3483
/ Sequence 3483, Application US/10487901
/ Publication No. US20050091708A1
/ GENERAL INFORMATION:
/ APPLICANT: Oreido, Jeremiah Vincent
/ APPLICANT: McCreery, David
/ APPLICANT: Pell, Randy
/ APPLICANT: Miller, Barbara
/ APPLICANT: Weglarz, Thadeus
/ APPLICANT: Gachotte, Daniel
/ APPLICANT: Blakelee, Beth
/ APPLICANT: Larrinua, Ignacio
/ APPLICANT: Reddy, Avutu
/ APPLICANT: Shukla, Vipula
/ APPLICANT: Crosley, Rodney
/ TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri
/ FILE REFERENCE: DOM-08552
/ CURRENT APPLICATION NUMBER: US/10/487,901
/ CURRENT FILING DATE: 2004-02-26
/ NUMBER OF SEQ ID NOS: 7560
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3483
/ LENGTH: 664
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-487-901-3483

Query Match 22.9%; Score 209.8; DB 21; Length 664;
Best Local Similarity 62.1%; Pred. No. 8.8e-45;
Matches 331; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

Qy 76 ATGGGGAGGGGAGAGATAGATTAATAAGATAGAGAAATCCAGCAAGCAAGTTTACA 135
Db 6 ATGGCGAGAGGAGAGATCCAGATCAGAGATAGAGAACAGCAAAACAGCAAGTACG 65
Qy 136 TATTCTAAGAGAGAGTTGGGATCTGAAGAGGCCAAGAGCTCACTGTTCTGTGAT 195
Db 66 TATTCAAGAGAGAAATGGTTTATTCAGAGAACACATGACTCAGCGTTTGTGTGAT 125
Qy 196 GCTCAGGTCTCTCATCATGTTCTCAAGCACAAGAAAGTTGGCTGATTACTGAGCCCC 255
Db 126 GCTAGGGTTTCATATCATGTTCTCAAGCTCCAAACAAGCTTCAATGATATACAGCCT 185
Qy 256 TCTACTGATATTAAAGGGATATATGAGAGTACCAAGTTGACTGCAATGATCTATG 315
Db 186 AACACCAACAGAGAGATGTAGATCTGACCAACTATTTCTGATGTCGATGTTGG 245
Qy 316 AATGCTCAGTATGAGAGATGCAATACGCTGAAGATCTGATGATTAACCAAAAC 375
Db 246 GCCACTCAATATGAGCGAATGCAAGAACCAAGAGAACTGTTGGAGACAAATAGAAAT 305
Qy 376 CTGAGAGAGAGATTAGAGAGAGAGAGGAGAAATTGAGGCACTAGCACTAAACAA 435
Db 306 CTCCGACTCAGATCAAGACAGAGCTAGGTGATGTTTGAAGCTTGAATCAAGAG 365
Qy 436 CTGCGGGCTTTGAGCAAACTTTGAAAGTCTCTTGAATGTTTGAAGCATAGAAAT 495
Db 366 CTGCGGTGTTTGAAGTGAATGAAACACTTTCAACTCGTTCCGAGCGCAAGTTC 425
Qy 496 CATGTATCGCCACACAACTGACCTTACAGAAAGAACTTAAGACAGAGGAAT 555
Db 426 AATCTCTTGGGAATCAGATCGAGACCAAGAGAAAGAAACAAAGTCAACAGACATA 485
Qy 556 TACCGGCTCTAATACATGAGTGAATGAAAGAGAGAAATCCGAACTACG 608
Db 556 TACCGGCTCTAATACATGAGTGAATGAAAGAGAGAAATCCGAACTACG 608

Db 486 CAAAAGATCTCATATCATGAGTGAATTAAGAGTGAAGATCTCACTATG 538

RESULT 14

US-10-487-901-7018
/ Sequence 7018, Application US/10487901
/ Publication No. US20050091708A1
/ GENERAL INFORMATION:
/ APPLICANT: Oreido, Jeremiah Vincent
/ APPLICANT: McCreery, David
/ APPLICANT: Pell, Randy
/ APPLICANT: Miller, Barbara
/ APPLICANT: Weglarz, Thadeus
/ APPLICANT: Gachotte, Daniel
/ APPLICANT: Blakelee, Beth
/ APPLICANT: Larrinua, Ignacio
/ APPLICANT: Reddy, Avutu
/ APPLICANT: Shukla, Vipula
/ APPLICANT: Crosley, Rodney
/ TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri
/ FILE REFERENCE: DOM-08552
/ CURRENT APPLICATION NUMBER: US/10/487,901
/ CURRENT FILING DATE: 2004-02-26
/ NUMBER OF SEQ ID NOS: 7560
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7018
/ LENGTH: 665
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-487-901-7018

Query Match 22.9%; Score 209.8; DB 21; Length 665;
Best Local Similarity 62.1%; Pred. No. 8.8e-45;
Matches 331; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

Qy 76 ATGGGGAGGGGAGAGATAGATTAATAAGATAGAGAAATCCAGCAAGCAAGTTTACA 135
Db 6 ATGGCGAGAGGAGAGATCCAGATCAGAGATAGAGAACAGCAAAACAGCAAGTACG 65
Qy 136 TATTCTAAGAGAGAGTTGGGATCTGAAGAGGCCAAGAGCTCACTGTTCTGTGAT 195
Db 66 TATTCAAGAGAGAAATGGTTTATTCAGAGAAACAGATGACTCAGCGTTTGTGTGAT 125
Qy 196 GCTCAGGTCTCTCATCATGTTCTCAAGCACAAGAAAGTTGGCTGATTACTGAGCCCC 255
Db 126 GCTAGGGTTTCATATCATGTTCTCAAGCTCCAAACAAGCTTCAATGATATACAGCCT 185
Qy 256 TCTACTGATATTAAAGGGATATATGAGAGTACCAAGTTGACTGCAATGATCTATG 315
Db 186 AACACCAACAGAGAGATGTAGATCTGACCAACTATTTCTGATGTCGATGTTGG 245
Qy 316 AATGCTCAGTATGAGAGATGCAATACGCTGAAGCATCTGAATGATTAACCAAAAC 375
Db 246 GCCACTCAATATGAGCGAATGCAAGAACCAAGAGAACTGTTGGAGACAAATAGAAAT 305
Qy 376 CTGAGAGAGAGATTAGAGAGAGAGAGGAGAAATTGAGGCACTAGCACTAAACAA 435
Db 306 CTCCGACTCAGATCAAGACAGAGCTAGGTGATGTTTGAAGCAAGCTTCAATTCAGAG 365
Qy 436 CTGCGGGCTTTGAGCAAACTTTGAAAGTCTCTTGAATGTTTGAAGCATAGAAAT 495
Db 366 CTGCGGTGTTTGAAGTGAATGAAACACTTTCAACTCGTTCCGAGCGCAAGTTC 425
Qy 496 CATGTATCGCCACACAACTGACCTTACAGAAAGAACTTAAGACAGAGGAAT 555
Db 426 AATCTCTTGGGAATCAGATCGAGACCAAGAGAAAGAAACAAAGTCAACAGACATA 485
Qy 556 TACCGGCTCTAATACATGAGTGAATGAAAGAGAGAAATCCGAACTACG 608
Db 486 CAAAAGATCTCATATCATGAGTGAATTAAGAGTGAAGATCTCACTATG 538

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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 6, 2005, 11:40:47 ; Search time 4399 Seconds

(without alignments)
2500.417 Million cell updates/sec

Title: US-10-690-246A-2

Perfect score: 1177
Sequence: 1 MGSKRIKIKIENPTNRQVT.....HPNPNLGIGYSHSLSLA 227

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPFO.spool/US10690246/runat_05102005_110910_6435/app_query.fasta_1.391
-DB=genembl -OPMT=faasp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000
-USER=US10690246@cgn 1 1 3731 @runat_05102005_110910_6435 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Genembl:*

1: gb ba:*\n2: gb hcg:*\n3: gb in:*\n4: gb om:*\n5: gb ov:*\n6: gb pat:*\n7: gb ph:*\n8: gb pl:*\n9: gb pr:*\n10: gb ro:*\n11: gb sts:*\n12: gb sy:*\n13: gb un:*\n14: gb vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1177	100.0	910	8	AY378149 Phalaenop
2	820	69.7	952	8	AB094964 Asparagus
3	802.5	68.2	1028	8	AY378147 Phalaenop
4	782.5	66.5	1005	8	AB071378 Lilium re

5	781.5	66.4	1039	8	AF503913 Lilium lo
6	758.5	64.4	980	8	AY378150 Phalaenop
7	755	64.1	1030	8	AY378148 Phalaenop
8	738	62.7	833	8	AF209729 Hemerocal
9	730.5	62.1	1002	8	AB094965 Thilipa ge
10	716	60.8	942	8	AY196350 Oncidium
11	701.5	59.6	1016	8	AB094966 Thilipa ge
12	700	59.5	938	8	AF230706 Tecoa cha
13	684.5	58.2	1084	8	AB003323 Oryza sat
14	684.5	58.2	1210	8	AK069317 Oryza sat
15	682.5	58.0	830	8	AY621154 Alpina h
16	675	57.3	1004	8	AF181479 Zea mays
17	675	57.3	1257	6	CO855034 Sequence
18	675	57.3	1257	6	CO855034 Sequence
19	664	56.4	1061	8	AF077760 Oryza sat
20	663	56.3	1166	8	AY541065 Hordeum v
21	653	55.5	959	8	AB007506 Triticum
22	651.5	55.4	852	8	AB050649 Magnolia
23	642	54.5	1083	8	AB107993 Triticum
24	641.5	54.5	830	8	AY397762 Chloranth
25	633.5	53.8	651	8	AY337751 Eupomatia
26	630.5	53.6	651	8	AY337750 Eupomatia
27	630.5	53.6	1008	8	AF052874 Papaver n
28	611	51.9	681	6	AR372458 Sequence
29	611	51.9	946	6	AR372458 Sequence
30	600.5	51.0	958	8	AF627631 Akebia tr
31	588	50.0	643	8	TAB577377 Akebia tr
32	582	49.4	896	8	AY627630 Akebia tr
33	579	49.2	809	8	AY436724 Petunia x
34	579	49.2	994	8	AF230704 Petunia x
35	576	48.8	828	8	ACA419959 Asarum ca
36	574	48.8	851	8	AY436723 Drimys wi
37	570	48.4	810	8	AY436725 Drimys wi
38	567.5	48.2	852	8	AY436715 Sarcoba he
39	565	48.0	906	8	GHY9724 Sarcoba he
40	562	47.7	935	8	AY436736 Lindera h
41	558	47.4	768	8	AY436722 Drimys wi
42	557.5	47.4	926	6	CO855038 Sequence
43	557.5	47.4	926	6	AX478039 Sequence
44	556	47.2	807	8	AY436737 Lindera e
45	555	47.2	834	8	ACA419955 Asarum ca

ALIGNMENTS

RESULT 1	AY378149	910 bp	mrna	linear	PLN 09-AUG-2004
LOCUS	AY378149	complete cds.			
DEFINITION	Phalaenopsis equestris MADS box transcription factor (MADS2) mRNA,				
ACCESSION	AY378149.1	GI:38680584			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Phalaenopsis equestris				
	Phalaenopsis equestris				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;				
	Epidendroideae; higher Epidendroideae; Vandaeae; Aeridinae;				
	Phalaenopsis.				
REFERENCE	1 (bases 1 to 910)				
AUTHORS	Tsai, W.C., Kuoh, C.S., Chuang, M.H., Chen, W.H. and Chen, H.H.				
TITLE	Four DEF-like MADS Box Genes Displayed Distinct Floral				
JOURNAL	Morphogenetic Roles in Phalaenopsis Orchid				
PUBMED	Plant Cell Physiol. 45 (7), 831-844 (2004)				
15295066					
REFERENCE	2 (bases 1 to 910)				
AUTHORS	Tsai, W.C., Chen, W.H. and Chen, H.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-SEP-2003) Department of Biology, National Cheng Kung				
	University, 1 University Rd., Tainan, Taiwan 701, Republic of China				
	Location/Qualifiers				
FEATURES	1..910				
source	/organism="Phalaenopsis equestris"				

[illegible]

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
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	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
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	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	68.18%	Indels:	3	
			Gaps:	2	

ORIGIN	Alignment Scores:	Prod. No.:	6.69e-65	Length:	1028
US-10-690-246a-2 (1-227) x AY378147 (1-1028)	Score:	802.50	Matches:	148	
	Percent Similarity:	85.90%	Conservative:	47	
	Best Local Similarity:	65.20%	Mismatches:	29	
	Query Match:	6			

ACCESSION AB071378
 VERSION AB071378.1 GI:20513259
 KEYWORDS
 SOURCE
 ORGANISM
 Lillium regale
 Lillium regale
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lillium.

REFERENCE
 1
 Winter, K. U., Weiser, C., Kaufmann, K., Bohne, A., Kirchner, C., Kanno, A., Saedler, H. and Theissen, G.
 Evolution of class B floral homeotic proteins: obligate heterodimerization originated from homodimerization
 Mol. Biol. Evol. 19 (5), 587-596 (2002)

JOURNAL
 MEDLINE
 PUBMED
 21959322
 11961093

REFERENCE
 2 (bases 1 to 1005)
 Kanno, A., Bohne, A., Saedler, H. and Theissen, G.
 Direct Submission
 Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi 980-8577, Japan (E-mail: kanno@life.tohoku.ac.jp, Tel: 81-22-217-5725 (ex. 5725), Fax: 81-22-217-5725)
 Location/Qualifiers

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ORIGIN

Alignment Scores:
 Pred. No.: 4.59e-63 Length: 1005
 Score: 782.50 Matches: 149
 Percent Similarity: 83.04% Conservative: 42
 Best Local Similarity: 64.78% Mismatches: 34
 Query Match: 66.48% Indels: 5
 DB: Gaps: 3

US-10-690-246a-2 (1-227) x AB071378 (1-1005)

QY 1 MecGlyargyllyysillegluilelylelyleluabnpzothrraenarglvalthr 20
 Db 10 ATGGGGGGGGAAGATCGAGATTAAAGATCGAAAATCGACGAATCGACAGTACT 69
 QY 21 TyserlysaargatvalgylileuulelylelylelylelyleuulaurvalleuCyasp 40
 Db 70 TATCCGAAGCGCCGACCGGAATCATCAAGAGCGACTGACTGCTGCTGTGAT 129
 QY 41 AlaglnvalserleuilemetpheserterthelgyllyleuualaaeplyrCyaserPro 60
 Db 130 GCCAGAGTCTCTCTCTATGTTCTCCAGCACCAGGAAGCTGTGAGAGTTCTGACGCC 189
 QY 61 SerthrapiileysgylilelyrgluargylrgrlvalvalThrsglymelaapleutp 80
 Db 190 TCACACACACGAAGAAATCTTGCACCGCTACACGACGCTGCGGAACTAACCTTGG 249
 QY 81 AsnaaglnlyrgrluargmetGlnaenThrleuylshleuAengluileAenglnasn 100
 Db 250 AGCGCGCAATCGAGAAATCGCAAAACATTTGAACATCTGACGAGATCAACCGCAC 309

QY 101 leuArglyeGluileargargyllygylugluileugluymecaspilleysgin 120
 Db 310 CTCGGAAAGAGATCGACCAAGATGGGGAGAGCTGATGATGATCACTCAAGAC 369
 QY 121 leuArgglyeugluinThrleugluinleuArglylevalarghisaarglytyr 140
 Db 370 CTCGGCGCTTGAAGCAAAATTTGACGAGCGCTCAAGCTGCTGCTCAAGAAAT 429
 QY 141 HlevalilealathrclnThrshapthryrlyrlylelylelylelyserthrargluthr 160
 Db 430 CAGTATATACACTCGACAGACTTCAAGAAAAGCTCAAAAATCTCGAAGAGCA 489
 QY 161 TyrArgAlaleuilehileugluene-----AspMetlyeGluilubnProaenlyr 177
 Db 490 CACAAACTTGCTGCTCCGTACCTCGGATATAGAGATTAAGATGAGATCAAGTCT 549
 QY 178 glyPheasnvalgluAenglnserargyletyrgluAenSerileProetValaenglu 197
 Db 550 GGTATGTAGACGAAAGACCCAGCAAC--TATGATGGCGGCTTGTCTGCGCAATGG 606
 QY 198 CysProGlnmecPheaserPheargvalValhileProaenglnProaenleuenglyleu 217
 Db 607 GCTTCTCATCTGTACAGAGTCCGA--GTCCAAAGCAGCCAGCAAACTGATGGGATG 663
 QY 218 gLyTYrGluSerHisaspLeuSerleuAla 227
 Db 664 GGTATGTGTTCCACGATCTCCGACTGGCT 693

RESULT 5
 AF503913 1039 bp mRNA linear PLN 13-MAY-2002
 LOCUS Lillium longiflorum MADS box protein (MADS1) mRNA, complete cds.
 DEFINITION
 AF503913
 VERSION
 AF503913.1 GI:20531752
 KEYWORDS
 Lillium longiflorum (Trumpet Lily)
 Lillium longiflorum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lillium.

REFERENCE
 1 (bases 1 to 1039)
 Tzeng, T.-Y. and Yang, C.-H.
 A MADS box gene from lily (Lillium longiflorum) is sufficient to generate dominant negative mutation by interacting with PISTILLATA (PI) in Arabidopsis thaliana
 Plant Cell Physiol. 42 (10), 1156-1168 (2001)

JOURNAL
 MEDLINE
 PUBMED
 21530302
 11673632

REFERENCE
 2 (bases 1 to 1039)
 Tzeng, T.-Y. and Yang, C.-H.
 Direct Submission
 Submitted (18-APR-2002) Institute of Biotechnology, National Chung Hsing University, 250 Kao-Kung Rd., Taichung, Taiwan 40227, ROC
 Location/Qualifiers

FEATURES
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 16..702
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ORIGIN

Alignment Scores:

Prod. No.: 5,9e-63 Length: 1039
 Score: 781.50 Matches: 149
 Percent Similarity: 83.04% Conservative: 42
 Best Local Similarity: 64.78% Mismatches: 34
 Query Match: 66.40% Indels: 5
 DB: 8 Gaps: 3

US-10-690-246a-2 (1-227) x AF503913 (1-1039)

QY 1 MetGlyArgGlyLeuIleGluIleLeuValIleGluAsnProThrAsnArgGlnValThr 20
 DB 16 ATGGGCGGGGAAAGATCGAGATTAGAGATTCAGAACTCGACGAATCCGACAGTCTACT 75
 QY 21 TySerIleValArgValGlyIleLeuValLeuValIleValGluLeuThrValIleCysAsp 40
 DB 76 TACTCGAAGCGCCGACCGGATCATCAGAGGCGAGCTGAGCTCAGCTGCTGTGAT 135
 QY 41 AlGlnValSerLeuIleMetPheSerSerThrGlyIleValIleAspTyrcysSerPro 60
 DB 136 GCGAGGTCTCTCTCTTATGTTCTCCAGCACCGGAAAGCTGTCTGAGATTCTGACAGCCC 195
 QY 61 SerThrAspIleValGlyIleTyrcyluArgTyrcyluValIleThrGlyMetAspLeuTrp 80
 DB 196 TCCACAGACAGAAAGATCTTCAGACCGCTACAGACGCTGTCCGGGATCAACCTCTGG 255
 QY 81 AsnAlaGlnTyrcyluArgMetGlnAsnThrIleuValIleValIleAsnGlnuIleAsnGlnAsn 100
 DB 256 AGCCGCGAATACGAAATGCAAAATGCAAAACCTTGAAACCTGACCGAGATCAATCGCAC 315
 QY 101 LeuArgIleGluIleArgArgIleGlyGluIleuGluGluGluGluGluGluGluGluGln 120
 DB 316 CTTCGCAAGAGATCAGCCAGAGATGGGGAGAGCTGATGATGATGATGATGATGATGATGAT 375
 QY 121 LeuArgIleGluGluGlnThrLeuGluGluSerLeuArgIleValIleGlnIleValIleGlnIleVal 140
 DB 376 CTGCGCGGTCTTGAGCAAAATTTGAGACGACGCTCAAGCTCGTTCGTCACCGCAGAGTAT 435
 QY 141 HisValIleAlaThrGlnThrAspThrTyrcyluValIleValIleValIleValIleValIleVal 160
 DB 436 CATGTGATGCAACTCTCAGACAGACTTACAAAGAAAGGCTCAAAATCTCGAAGAAACCA 495
 QY 161 TyrArgAlaLeuIleIleGluLeu-----AspMetIleGluGluAsnProAsnTyrc 177
 DB 496 CACAGAACTTCTCTCGGACCTGTGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAT 555
 QY 178 GlyPheAsnValGluAsnGlnSerArgIleTyrcyluAsnSerIlePheMetValIleAsnGlu 197
 DB 556 GATTATGAGACGAAAGACCCAGCAAC---TATGATGCGCGCTGTGCTGCGCAATGGG 612
 QY 198 CysProGlnMetPheSerPheArgValIleIleProAsnGlnProAsnLeuGluIleu 217
 DB 613 GCTTCTCATCTGTCAGAGCTTCGA---GTCCAAACCGACCGCAACCTGCAATGGGATGG 669
 QY 218 GlyTyrcyluSerHisAspLeuSerLeuAla 227
 DB 670 GGTATGCTCCCATGATCTCCGACTGGCT 699

RESULT 6
 AY378150 980 bp mRNA linear PLN 09-AUG-2004
 LOCUS Phalaenopsis equestris MADS box transcription factor (MADS3) mRNA,
 DEFINITION complete cds.
 VERSION AY378150
 ACCESSION AY378150.1 GI:36680586
 KEYWORDS
 SOURCE
 ORGANISM
 Phalaenopsis equestris
 Phalaenopsis equestris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 Epidendroideae; higher Epidendroideae; Vandaeae; Aeridinae;

REFERENCE

1 (bases 1 to 980)
 Tseai, W.C., Kuo, C.S., Chuang, M.H., Chen, W.H. and Chen, H.H.
 Four DEF-Like MADS Box Genes Displayed Distinct Floral
 Morphogenetic Roles in Phalaenopsis Orchid
 Plant Cell Physiol. 45 (7), 831-844 (2004)
 JOURNAL
 PUBMED 15295066
 REFERENCE
 AUTHORS
 Tseai, W.C., Chen, W.H. and Chen, H.H.
 TITLE
 Direct Substitution
 Submitted (02-SEP-2003) Department of Biology, National Cheng Kung
 University, 1 University Rd., Tainan, Taiwan 701, Republic of China
 JOURNAL
 location/Qualifiers

FEATURES

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 LRLA"

ORIGIN

Alignment Scores:

Prod. No.: 7,36e-61 Length: 980
 Score: 758.50 Matches: 142
 Percent Similarity: 81.94% Conservative: 44
 Best Local Similarity: 62.56% Mismatches: 36
 Query Match: 64.44% Indels: 5
 DB: 8 Gaps: 2

US-10-690-246a-2 (1-227) x AY378150 (1-980)

QY 1 MetGlyArgGlyLeuIleGluIleLeuValIleGluAsnProThrAsnArgGlnValThr 20
 DB 196 ATGGGCGGGGAAAGATCGAGATTAGAGATTCAGAACTCGACGAATCCGACAGTCTACT 255
 QY 21 TySerIleValArgValGlyIleLeuValLeuValIleValGluLeuThrValIleCysAsp 40
 DB 256 TACTCGAAGCGCGCTGAGATCATGAAAGGCGAGCTCACGATTCTCTGTGAT 315
 QY 41 AlGlnValSerLeuIleMetPheSerSerThrGlyIleValIleAspTyrcysSerPro 60
 DB 316 GCTACGCTCTCCCTTGTATGTTCTCCAGCACCGGAAAGCTTCCGAGTATTGATGCTCT 375
 QY 61 SerThrAspIleValGlyIleTyrcyluArgTyrcyluValIleThrGlyMetAspLeuTrp 80
 DB 376 ACCACCGATGCCAAGATGATATGATCGTTACAGACGAGTGTCCGCAATAAATTATGG 435
 QY 81 AsnAlaGlnTyrcyluArgMetGlnAsnThrIleuValIleValIleValIleValIleValIleVal 100
 DB 436 AGCAGACGATACGAAAGATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATG 495
 QY 101 LeuArgIleGluIleArgArgIleGlyGluIleuGluGluGluGluGluGluGluGluGln 120
 DB 496 TTGAGAGGAGATTAAGCAGAGATGCGGAGAGATTTTAAAGGCTTAAGAAATCAAGAA 555
 QY 121 LeuArgIleGluGluGlnThrLeuGluGluSerLeuArgIleValIleGlnIleValIleGlnIleVal 140
 DB 556 CTGCGTGTCTTGAGCAAAATGATGACAGAGCCCTTAAGCTTGTAAAGAAATCGAAAGTAT 615
 QY 141 HisValIleAlaThrGlnThrAspThrTyrcyluValIleValIleValIleValIleValIleVal 160

D6		616	CACGTCATCAGACACCAGACAGATACATTCAAAAAGTTGGAAAACTGTCAAAGAAAC	675
OY		161	TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluValProAsnTyrGlyPheAsn	180
D6		676	CACAGGAACCTACTCCGGGAGCTG-----GAAACTGAGCACGCCGCTTACTAC	723
OY		181	ValGluAsnGlnSerHisGlyIleTyrGluAsnSerIlePheMetValAsnGluCyPrroGln	200
D6		724	GTTGATGATGATGCCAACCACTGATGATCGCCGCTTGACCTGGAAATGGGGCTTCCCTAC	783
OY		201	MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyTyrGly	220
D6		784	TTGRTTATTATTTCGT--ACCCAACAAGCCAGCCGAACTTTCAGGGAGTTGATATGTC	840
OY		221	SerHisAspLeuSerLeuAla	227
D6		841	CCTCATGATCTACGCTCGCC	861
RESULT 7				
AY378148			1030 bp mRNA linear	PLN 09-AUG-2004
LOCUS			Phlaenopsis equestris MAD55 transcription factor (MAD5) mRNA,	
DEFINITION			Complete cds.	
ACCESSION		AY378148		
VERSION		AY378148.1	GI:45935300	
KEYWORDS				
SOURCE				
ORGANISM			Phlaenopsis equestris	
			Phlaenopsis equestris	
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			Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;	
			Epidendroideae; higher Epidendroideae; Vandaeae; Neolidine;	
			Phlaenopsis.	
REFERENCE			1 (bases 1 to 1030)	
AUTHORS			Tsai,W.C., Khoo,C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.	
TITLE			Four DEF-like MAD5 Box Genes Displayed Distinct Floral	
JOURNAL			Morphogenetic Roles in Phlaenopsis Orchid	
PUBMED			Plant Cell Physiol. 45 (7), 831-844 (2004)	
PUBID			15295066	
REFERENCES			2 (bases 1 to 1030)	
AUTHORS			Tsai,W.C., Chen,W.H. and Chen,H.H.	
TITLE			Direct Submission	
JOURNAL			Submitted (02-SEP-2003) Department of Biology, National Cheng Kung	
			University, 1 University Rd., Tainan, Taiwan 701, Republic of China	
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ORIGIN				
Alignment Scores:				
Fred. No.:		1.64e-60	Length:	1030
Score:		755.00	Matches:	149
Percent Similarity:		82.59%	Conservative:	36
Best Local Similarity:		66.52%	Mismatches:	29
Query Match:		64.15%	Indels:	10
DB:		8	Gaps:	2

US-10-690-246A-2 (1-227) x AY378148 (1-1030)

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OY      1 MetGlyArgGlyLysIleGluIleLysLysIleGluAsnProThrAsnAlaGlnValThr 20
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OY      21 TyrSerLysAspArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
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OY      41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
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OY      61 SerThrAspIleLysGlyIleTyrGluLysArgTyrGlnValAlaThrGlyMetAspLeuTrp 80
Db      435 TCCACAGACGTTAAAGATATAAGTTGAGAGAGTACCAGAAATTTACCCGAAATGATATATGG 494
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Db      495 GATCGCAATATTCAGAGAGATTCAGAACACTCTGAGGAATCTCAGGAGATTAATCGTAAT 554
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Db      555 CTTCAAGAGGAGATTAAGACAGAGAGAAAGGGAGAAATCTGAAAGGGTTGGCGCTTAAAGAG 614
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Db      615 CTGGCGCGCTCTTGGACAAAAATTGGAGAGAGTGGTTAAGATTGTTGGCGACAGAAAGTAT 674
OY      141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
Db      675 CATGTGATCGGTACGCAAAACAGACACTTGGACGGAAAGCTCAAAAGCACACAGCAATA 724
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Db      735 TACAGAGCCCTTAACGCACTGAACCTGCACAAAGCTGCACAAAGATCAACCGTCACAGTTT 794
OY      180 AsnValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysPro 199
Db      795 CTCGTAGAAGATCTTAAGCTGCATTTAAGACAGCTCAATCTCAATGCCAATTCGG----- 848
OY      200 GlnMetPheSerPheArgValAlaHisProAsnGlnProAsnLeuGluLysGlyTyr 219
Db      849 -----CTGCACCGGAGTGACGCCAATGTCAGAAATGATGCT 887
OY      220 GluSerHisAsp 223
Db      888 GAGTGTCAATGAG 899

RESULT 8
LOCUS   AF209729                833 bp    mRNA    linear    PLN 01-DEC-2000
DEFINITION   HemeroCALLIS hybrid cultivar putative MADS box transcription factor
              (MADS1) mRNA, complete cds.
ACCESSION   AF209729
VERSION     AF209729.1    GI:11494136
KEYWORDS
SOURCE      HemeroCALLIS hybrid cultivar (daylily)
AUTHORS     HemeroCALLIS hybrid cultivar
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
            Hemerocallidaceae; HemeroCALLIS.
REFERENCE   1 (bases 1 to 833)
            Lange,N.E.
            Molecular changes during the expansion and senescence of
            ethylene-insensitive daylily flowers
            Thesis (1999) University of California, Davis
            Lange,N.E., Valpuesta,V., Napoli,C.A., Labavitch,J.M. and Reid,M.S.
            Direct Submission
            Submitted (30-NOV-1999) Environmental Horticulture, University of

```


ORIGIN

Alignment Scores:

Pred. No.: 1.78e-55 Length: 938
 Score: 700.00 Matches: 130
 Percent Similarity: 84.08% Conservative: 39
 Best Local Similarity: 64.68% Mismatches: 30
 Query Match: 59.47% Indels: 2
 DB: 8 Gaps: 2

US-10-690-246a-2 (1-227) x AF230706 (1-938)

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 DB 4 GGGATCATGAAAGAGCGCAAGAGCTCAAGCTCTTGGCAATCTGAAGCTTCTATAC 63
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 QY 47 MetPheSerSerThrGlyLeuLeuAlaAspTyrCysSerProSerThrAspIleYsGly 66
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 DB 64 ATGTTCTCCAGCACTGGCGCAAGTTCCGCCAGTACAGTCTTCCACCGATACGAAAGAG 123
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 QY 67 IleTyrGluYsGlyTyrGlnValValThrGlyMetAspLeuThrAspAlaGlnTyrGluYs 86
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 DB 124 GTTTAGCATCGGATCGCAAGAGTGAATGCACTGTGGAGTTCCGAGTTCAGAGAGG 193
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 QY 87 MetGlnAsnThrLeuYsYsIleLeuAsnGluIleAsnGlnAsnLeuYsGlyLeuYs 106
 |||:::|||||
 DB 184 ATGCAAAATAACTGATCATCTGGAGAGATCAACCGAAATCTTCCAGAGCAATTAAGG 243
 |||:::|||||
 QY 107 ArgArgLeuGlyGluGluLeuGluGlyMetAspIleYsGlnLeuYsGlyLeuGluGln 126
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 DB 244 CAAGAGCGGCGCAAGAGTCTTGACGGCTTGACATCAAAAGCTGCTGTGGTGAAGCA 303
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 QY 127 ThrLeuGluLeuSerLeuYsGlyIleValArgHisArgYsGlyThrValIleAlaThrGln 146
 |||:::|||||
 DB 304 AATGTGATGAGCTTTGAGGATTTGTCGTCAAAGAAATATCATGTTATCAACCAACAG 363
 |||:::|||||
 QY 147 ThrAspThrTyrLeuYsYsLeuYsSerThrArgGluThrTyrArgAlaLeuIleHis 166
 |||:::|||||
 DB 364 ACCGATATCATATAAAGAGAGCTGAAGAAATTCCTCAATCACTCAAGAACTTAATGCGA 423
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 QY 167 GlnLeuAspMetLeuYsGluGluAsnProAsnTyrGlyPheAsnValGluAsnGlnSerArg 186
 |||:::|||||
 DB 424 GAACCTGAGATGAGAGATGAGACCCAGTTACGGGGTTC---GTCCGCAATGATTCCTACT 480
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 QY 187 IleTyrGluAsnSerIlePheMetValAsnGluCysProGlnMetPheSerPheArgVal 206
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 DB 481 AACTTACGACAGCGCTCTGGCACTGGCAATGCTGGGTCTCATGTCTACGGGTACCGT--- 537
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 QY 207 ValHisProAsnGlnProAsnLeuLeuGlyLeuGlyTyrGluSerHisAspLeuSerLeu 226
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 DB 538 GTTCAGCAAGCAAGCGCAATCTCCATGGAATAGGCTCTCATATGACTTTCGCGCTG 597
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 QY 227 Ala 227
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 DB 598 GCA 600
 |||

RESULT 13
 AB003323 1084 bp mRNA linear PLN 21-MAR-2002
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) mRNA for MADS box-1like
 protein, complete cds, clone:E20969.

ACCESSION
 AB003323
 VERSION
 AB003323.1 GI:5295979
 KEYWORDS
 MADS box-1like protein.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Rharioideae; Oryzaceae; Oryza.
 REFERENCE
 1 Shinozuka, Y., Yamamoto, K. and Sasaki, T.
 TITLE
 Characterization of rice MADS box-1like genes
 JOURNAL
 Unpublished

REFERENCE 2 (bases 1 to 1084)
 AUTHORS
 Sasaki, T.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (23-APR-1997) Takuji Sasaki, National Institute of
 Agricultural Resources, Rice Genome Research Program, Kamondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@abr.affrc.go.jp, Tel:0298-38-7441,
 Fax:0298-38-7468)

FEATURES

source

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CDS

Alignment Scores:
 Pred. No.: 5.69e-54 Length: 1084
 Score: 684.50 Matches: 138
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 Best Local Similarity: 60.79% Mismatches: 50
 Query Match: 58.16% Indels: 5
 DB: 8 Gaps: 5

ORIGIN

US-10-690-246a-2 (1-227) x AB003323 (1-1084)
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 DB 102 ATGGGAGAGGGCAAGATCGAAGATCAAGCGGATCGAGAACGCCAACAGGAGGTGACC 161
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 QY 21 TyrSerLeuArgArgValGlyIleLeuYsYsAlaYsGluLeuThrValLeuCyAAsp 40
 |||:::|||||
 DB 162 TACTGAAAGCGCGCACGGGATCATGAAGAGCCAGGAAGCTCACTGCTGCGAC 221
 |||:::|||||
 QY 41 AlaGlnValSerLeuIleMetPheSerThrGlyYsLeuAlaAspTyrCysSerPro 60
 |||:::|||||
 DB 222 GCCCAGGTGCCATCATCATGTTCTCTCCACCGGCAAGTACACAGATTCTGACAGCCT 281
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 QY 61 SerThrAspIleYsGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
 |||:::|||||
 DB 282 TCACCGACATCAAGAGGATCTTTGACGCTACACGAAGCCATCGGACCAAGCTTTGG 341
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 QY 81 AsnAlaGlnTyrGluYsMetGlnAsnThrLeuYsYsIleLeuAsnGluIleAsnGlnAsn 100
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 DB 342 ATCGACGATATGAAGATATGCAAGCGCAGCTGAGCATCTCAAGACATCAACCGCAAC 401
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 QY 101 LeuArgYsGluIleArgArgArgYsGlyGluGluLeuGluGlyMetAspIleYsGln 120
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 DB 402 CTGCGCAGCAGATCGAGCAAGAGATGGAGAAGATCTGACGCGGTGAGTTCCGACGAG 461
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 QY 121 LeuArgYsGluGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgYsTyr 140
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 DB 462 CTGGCGGCTTTGAGGAAATATGATCGCGCTTCACAGAGGTTTCGACAGGAAGTAT 521
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 QY 141 HisValIleAlaThrGlnThrAspThrTyrYsYsLeuLeuYsSerThrArgGluThr 160
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 DB 522 CATGTATCAACCAAGCATGAACCTTCAAGAAAGGTGAAGACTCTCAACGAGGG 581
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 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetYsGluGluAsnProAsnTyrGlyPheAsn 180
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Qy 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCyPProGln 200
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636 GTGACGACACACCGGCGCGGCTGGAGACGGCGGCGCGC---GCCGCGCGGCGCGCGAC 692

Db 201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLeuGlyTyr--- 219
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693 ATGTCGCGCTTCGCGCGGTGG---CCGACGCGACCGCACTGCACGCGCATGGCTACGCGC 749

Qy 220 GluSerHisAspLeuSerLeu 226
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750 GGCACACGACGACCTCGCGCTTC 770

RESULT 14
AK069317
LOCUS
DEFINITION
AK069317 1210 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023014M24, full
insert sequence.
ACCESSION
AK069317
VERSION
AK069317.1 GI:32979341
KEYWORDS
FLI cDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriharoidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
1 The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,M., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Oato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice (5631), 376-379 (2003)

JOURNAL
MEDLINE
PUBMED
2752273
AUTHORS
2 (bases 1 to 1210)
12869764
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T.,
Hori,F., Hotta,I., Iida,J., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Matsuda,H., Matsubara,K., Matsuyama,T., Mura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Nishikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Ooto,N., Ota,Y., Otono,Y., Ryu,R., Satoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,T., Tagami,Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission

JOURNAL
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nae.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Matsuda,H., Mura,J.,
Mizuno,K., Narikawa,R., Nishikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken
Adachi,J., Aizawa,K., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
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Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,T., Tagami,Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
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FEATURES
source
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/clone="J023014M24"

ORIGIN
Alignment Scores:
Pred. No.: 6,46e-54 Length: 1210
Score: 684.50 Matches: 138
Percent Similarity: 75.77% Conservative: 34
Best Local Similarity: 60.79% Mismatches: 50
Query Match: 58.16% Indels: 5
DB: 8 Gaps: 5

US-10-690-246A-2 (1-227) x AK069317 (1-1210)

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Qy 41 AlAGlnValSerLeuIleMetPheSerSerThrGlyIleLeuAlaAspTyrCySerPro 60
336 GCCCAGGTCCCATCAATCAATGTTCTCTCCACCGGCAAGTACACGAGTTCTGACGCTT 395

Db 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
396 TCCACCGACATCAAGGGGAGATCTTACCGCTTACGACGACCATCGCACCAGCTTTGG 455

Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuValIleLeuAsnGluIleAsnGlnAsn 100
456 ATGAGCAGATGTGAGATATGACGCGCAGCTGAGCATCTCAAGGACATCAACGCGAAC 515

Db 101 LeuArgIleGluIleArgArgArgIleGlyIleGluIleLeuGluIleGluMetAspIleLeuGln 120

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: October 6, 2005, 10:27:46 ; Search time 558 Seconds
(without alignments)
2408.210 Million cell updates/sec

Title: US-10-690-246A-2

Sequence: 1 MRRGKRIEIKIENPTNRQVT.....HPNQPVLLGIYSHSLSLA 227

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: geneseqn2000s:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	675	57.3	1257	ADJ42257	Aad42257 Corn AP3
3	675	57.3	1257	ADJ42278	Adi04278 Corn AP3
4	611	51.9	681	AAF85393	Aaf85393 Nucleicid
5	611	51.9	946	AAF85392	Aaf85392 Nucleicid

6	611	51.9	946	ABR88485	ABR88485 Poplar pr
7	611	51.9	946	ACA62518	ACA62518 Poplar ho
8	595	50.6	924	AA57943	AA57943 Poplar fl
9	576	48.9	637	ADK59650	Adk59650 Plant DNA
10	557.5	47.4	926	ADJ42259	Adj42259 Soybean A
11	557.5	47.4	926	ADJ42282	Adj42282 Soybean A
12	528.5	44.9	644	ACN53850	ACN53850 Cotton an
13	528	44.9	882	AAQ51189	AAQ51189 Homeotic
14	526.5	44.7	982	AA600104	AA600104 Plant DNA
15	521.5	44.3	630	ADK59791	Adk59791 Plant DNA
16	509.5	43.3	664	ADK56100	Adk56100 Plant DNA
17	509.5	43.3	665	ADK59635	Adk59635 Plant DNA
18	509.5	43.3	954	ACN51525	ACN51525 Arabidops
19	509.5	43.3	988	ADJ42259	Adj42259 Soybean A
20	509.5	43.3	988	ADJ42282	Adj42282 Soybean A
21	507.5	43.1	959	AAQ40831	AAQ40831 Arabidops
22	486	42.1	989	AAQ55879	AAQ55879 Eucalyptu
23	485	41.2	954	ACN40685	ACN40685 Arabidops
24	480	40.8	498	ADP95468	ADP95468 Cotton ex
25	432	36.7	951	ADJ61340	Adj61340 Cotton cd
26	427.5	36.3	639	ACN53901	ACN53901 Cotton an
27	415.5	35.2	868	AAQ00103	AAQ00103 Cotton an
28	414	35.2	425	ADQ03168	ADQ03168 Arabidops
29	413	35.1	649	ACN54118	ACN54118 Cotton an
30	412	35.0	407	ADQ06448	ADQ06448 Soybean t
31	406	34.5	601	ACN58761	ACN58761 Cotton gy
32	400	34.0	896	ADJ55880	Adj55880 Thalecres
33	400	34.0	914	ADJ001642	Adj001642 Thalecres
34	400	34.0	914	ADJ001642	Adj001642 Thalecres
35	400	34.0	914	ADJ001642	Adj001642 Thalecres
36	399	33.9	632	ADK55993	ADK55993 Plant DNA
37	397	33.7	742	ADK56091	ADK56091 Plant DNA
38	393	33.4	474	ADP95556	ADP95556 Cotton ex
39	391.5	33.3	674	ADK56104	ADK56104 Plant DNA
40	386	32.8	401	ADQ03170	ADQ03170 Arabidops
41	386	32.8	432	ADQ03170	ADQ03170 Arabidops
42	385	32.7	780	AAQ55089	AAQ55089 fbp1 cdna
43	382.5	32.5	535	ADP94271	ADP94271 Cotton ex
44	378	32.1	909	ACG35208	ACG35208 Arabidops
45	371.5	31.6	1089	AAQ42258	AAQ42258 Corn AP3

ALIGNMENTS

RESULT 1
ADJ44530 standard; cDNA; 681 BP.
XX ADJ44530;
XX AC ADJ44530;
XX DT 06-MAY-2004 (first entry)
XX DB Plant cDNA #5530.
XX KW Plant; gene; seq; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX OS Eukaryota.
XX PN US2004016025-A1.
XX PD 22-JAN-2004.
XX PF 26-SEP-2002; 2002US-00260238.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.

CC present invention.

XX Sequence 1257 BP; 320 A; 353 C; 340 G; 244 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,73e-62	Length:	1257
Score:	675.00	Matches:	135
Percent Similarity:	75.11%	Conservative:	37
Best Local Similarity:	58.95%	Mismatches:	51
Query Match:	57.35%	Indels:	6
DB:	13	Gaps:	5

US-10-690-246a-2 (1-227) x ADR04278 (1-1257)

```

QY      1 MetGlyArgGlyValIleGluIleValIleGluAsnProThrAsnArgGlnValThr 20
        |||||
DB      131 ATGGGGCGGGCAAGATCGAGATCAAGCGGATCGAAGAACCCCAACAGCCGCAAGTGAAC 190
        |||||
QY      21 TyrSerIleArgArgValGlyIleLeuValAlaValGluLeuThrValIleuCyAsp 40
        |||||
DB      191 TACTCGAAGCGCGGACGGGATCATGAAAGAGCCGCGACGCTCACCGCTCTCGAC 250
        |||||
QY      41 AlaGlnValSerIleuIleuMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
        |||||
DB      251 GCCCAGGTGCGCATCATGATGTTCTCTCCACCGGCAAGTACCAAGATCTGCAAGCCC 310
        |||||
QY      61 SerThrAspIleuValGlyIleTyrGlnArgTyrGlnValValThrGlyMetAspLeuTyr 80
        |||||
DB      311 GGAACCGACATCAAGACCATCTTGAACCGGTACAGAGCCATCGGACCAAGCTATGG 370
        |||||
QY      81 AsnAlaGlnTyrGlnArgMetGlnAsnThrIleuValIleuAsnGlnIleAsnGln 100
        |||||
DB      371 ATGACGACAGTATGAATATGACCGGACCGCATCTCAAGACATCATCGTGTG 430
        |||||
QY      101 LeuArgValGluIleArgArgValGlyGluGluLeuGluGluMetAspIleValGln 120
        |||||
DB      431 CTCGCGACAGAGATTAGGCAAAAGATGCGGACGAGATCGACAGTCTGCACTTCAAG 490
        |||||
QY      121 LeuArgGlyValGluIleGlnThrLeuGluGluSerLeuArgIleValArgHisArgValTyr 140
        |||||
DB      491 CTCGCGGCGCTCAAGCAAAAGTCTGACGCGGCTCTCAAGAGGTGCTGCAATAGAAAGTAC 550
        |||||
QY      141 HisValIleIleThrGlnThrAspThrTyrValValLeuValLeuValSerThrArgGluThr 160
        |||||
DB      551 CATGTATCATGACGACGACGATGATCTACTACAAAGAAAGTGAAGCATCGCAGAGCGG 610
        |||||
QY      161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluGluAsnProAsnTyrGlyPheAsn 180
        |||||
DB      611 TACAAAGAACCTGACAGCAGAGCTAGGCATCGGAGAGAC---CCGCGGTCTGGGTAC--- 664
        |||||
QY      181 ValGluAsnGlnSerArg-----IleTyrGluAsnSerIleProMetValAsnGluCys 198
        |||||
DB      665 GTGGACAACACGGGCGCGGCGTGCCTGGGACGCGCGGCGGCGGCGGCGGCGGCGG 724
        |||||
QY      199 ---ProGlnMetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLeu 217
        |||||
DB      725 CCGCGGACATGATACCGCTTCCGCGTGTG---CCACGCAAGCCCAACCTGACGCGGATG 781
        |||||
QY      218 GlyTyrGluSerHisAspLeuSerLeu 226
        |||||
DB      782 GCCTACGGCTTCAACGACCTCCGCGCTG 808
        |||||

```

RESULT 4

AAF85393 standard; cDNA; 681 BP.

AAF85393;

23-JUL-2001 (first entry)

Nucleotide sequence of the floral homeotic protein PTD.

Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;

KW LEF; FLORICANDUA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KM fertility; sterility; se.
 XX

OS Populus balsamifera.

Key	Location/Qualifiers
FT CDS	1..681
FT	/*tag= a
FT	/product= "PTD"

CA2319853-A1.

01-APR-2001.

02-OCT-2000; 2000CA-02319853.

01-OCT-1999; 99US-00410464.

(UYOR-) UNIV OREGON HEALTH SCI.

Rottman WH, Strauss SH, Brunner AM, Sheppard LA;

WPI, 2001-336098/36.

P-PSDB; AAB68435.

Novel isolated polynucleotide derived from Populus species, useful for

producing transgenic plants having modified fertility characteristic,

particularly sterility.

Claim 25; Page 42-43; 69pp; English.

The present sequence encodes a floral homeotic protein, designated PTD.

It is derived from Populus balsamifera subsp. erichocarpa. The

specification also describes PTLF, PTAG-1 and PTAG-2 proteins. The floral

homeotic proteins are expressed in floral tissues. PTLF is a homologue of

LEAFY (LFY) and FLORICANDUA (FLO), and is expressed in immature

inflorescences on which floral primordia are developing. PTD is a

homologue of DEFICIENS (DEF), and is strongly expressed in stamen

CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are

homologues of AGAMOUS (AG). The floral homeotic proteins and

polynucleotides are useful for producing transgenic plants having

modified fertility characteristics, particularly sterility

Sequence 681 BP; 228 A; 148 C; 157 G; 148 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.68e-56	Length:	681
Score:	611.00 <td>Matches:</td> <td>128 </td>	Matches:	128
Percent Similarity:	70.69% <td>Conservative:</td> <td>36 </td>	Conservative:	36
Best Local Similarity:	55.17% <td>Mismatches:</td> <td>56 </td>	Mismatches:	56
Query Match:	51.91% <td>Indels:</td> <td>12 </td>	Indels:	12
DB:	4	Gaps:	4

US-10-690-246a-2 (1-227) x AAF85393 (1-681)

```

QY      1 MetGlyArgGlyValIleGluIleValIleGluAsnProThrAsnArgGlnValThr 20
        |||||
DB      1 ATGGGTCTGCGAAGATTGAATCAAGAGATCGAAGAACCCCAACAGGCAAGTCAAC 60
        |||||
QY      21 TyrSerIleArgArgValGlyIleLeuValAlaValGluLeuThrValIleuCyAsp 40
        |||||
DB      61 TACTCGAAGAGAAAGTATTTTCAAGAAAGCCCAAGAACTCATCTTGTGTGAT 120
        |||||
QY      41 AlaGlnValSerIleuIleuMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
        |||||
DB      121 GCTAAGTCTCTTATCATGTTCTTCCACACATCAACAACTGAAGTACATTAGCCCC 180
        |||||
QY      61 SerThrAspIleuValGlyIleTyrGlnArgTyrGlnValValThrGlyMetAspLeuTyr 80
        |||||
DB      181 TCCACATCGACAAGAGATCTACATCAATTCAGAACGCTTACGATATCTGTGG 240
        |||||
QY      81 AsnAlaGlnTyrGlnArgMetGlnAsnThrIleuValIleuAsnGlnIleAsnGln 100
        |||||

```


ID	ABK88485	standard; cDNA; 946 BP.
XX		
AC	ABK88485;	
XX		
DT	29-AUG-2003	(revised)
DT	07-OCT-2002	(first entry)
XX		
DE	Poplar protein transduction domain, PTD, cDNA.	
XX		
KW	Poplar; <i>sp</i> ; gene; plant; DEFICIENS; transgenic; promoter;	
KW	protein transduction domain; floral homeotic gene;	
KW	floral-specific expression; cytochrome; fertility; sterility; PTLF;	
KW	PTAG-1; PTAG-2.	
XX		
OS	Populus balsamifera; subsp. trichocarpa.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..684
FT		/*tag= a
FT		/product= "PTD"
XX		
EN	USG39592-B1.	
XX		
PD	28-MAY-2002.	
XX		
PE	01-OCT-1999; 99US-00410464.	
XX		
PR	06-APR-1998; 98US-0080851P.	
PR	06-APR-1999; 99US-00287700.	
XX		
PA	(UYOR-) UNIV OREGON HEALTH SCI.	
XX		
PI	Strauss SH, Rotmann W, Brunner A, Sheppard L;	
XX		
DR	WPI; 2002-572853/61.	
XX		
DR	P-PSDB; ABG30865.	
XX		
PT	New protein transduction domain promoter nucleic acid molecule useful for	
PT	producing transgenic plants having modified fertility characteristics,	
PT	particularly sterility.	
XX		
PS	Example 1; Col 35-38; 46pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid molecule especially a	
CC	protein transduction domain (PTD) promoter; (i) that hybridizes under	
CC	wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium	
CC	dodecyl sulphate) at 65 plusoc to nucleotides or (ii) comprising 35	
CC	consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene	
CC	and is the homologue of DEFICIENS. Also includes are a recombinant	
CC	nucleic acid comprising the PTD promoter, a cell transformed with the	
CC	recombinant nucleic acid and a transgenic plant comprising the	
CC	transformed cell. The PTD promoter is useful to obtain floral-specific	
CC	expression of genes such as cytokinins, that are employed in genetic	
CC	ablation strategies to produce trees having modified fertility	
CC	characteristics, including sterility. Genetic constructs comprising	
CC	antisense versions or dominant negative mutants of PTD are useful in	
CC	producing genetically engineered Poplars and other trees, and for sense	
CC	suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1 and	
CC	PTAG-2 (none are defined). The present sequence is the PTD cDNA. (Updated	
CC	on 29-AUG-2003 to standardise OS field)	
XX		
XX		
SQ	Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;	
XX		
Alignment Scores:		
Pred. No.:	8.68e-56	Length: 946
Score:	611.00	Matches: 128
Percent Similarity:	70.69%	Conservative: 36
Best Local Similarity:	55.17%	Mismatches: 56
Query Match:	51.91%	Indels: 12
DB:	6	Gaps: 4
US-10-690-246A-2 (1-227) x ABK88485 (1-946)		

QY		MetGLYARGSLYVLIIGLNIIELYSVSLIEGLIUSANPQFIRANASRGINVAITNR	20
Db		1 ATGGGTCGTGGAAAGTTGSAATCAAGAAAGTCAAAAACCCCAACAGGACATCACC	60
QY		21 TYSETLYSARARGLVIGLYILEULYSLYSLALYSGLIUEUTHVALIEUCYASAP	40
Db		61 TATCGAAGAGAAAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCATGTACTTGGAT	120
QY		41 ALGILVALISERLEULIEMECHESESERTHGLYLYLEULALAPRYCYSSERPRO	60
Db		121 GCTAAGGTCTCTTATCATGTCTTCACAACTCAACAACTCAATGATGATCATTAAGCCC	180
QY		61 SETTHASPLILEYGLYILEYTCGLYARGYRGINVAIVALTHRGIMESAPLEUTRP	80
Db		181 TCCACATCCACAAGAAAGATCTTACCATCAATATACAAACGCTTTAGGCATAGATCTGTGG	240
QY		81 ASNALAGLNTYRGILYARGWECGLINABNTHREULYSHISLEUANGIUILEANGINASN	100
Db		241 GGCACCTCAATACGAGAAATGCGAAGAGCATTTGAGGAAGCTGAATGATATCAATCATTAAG	300
QY		101 LEUARGLYSGLIULEARGARGRLYSGLYGLIUGLIUGLIUGLIYMETASPLILEYSGIN	120
Db		301 CTGAGACAAAGAAATCAGCGACAGAGAGAGAGAGGCGCTGATGATCTGACCATGTATCAT	360
QY		121 LEUARGLYLEUGLIUGLINTHREUGLIUGLISERLEUARGHISARGLYSRYR	140
Db		361 CTGCGGGCTTGAGCAACATATGACTCAACCTTGAAATGGTGGCTGGCAGGAGATAC	420
QY		141 HIEVALIIEALATHRGINTHRASPTHTYRILYSLYSLYSEULYSEERTHRRARGIUTHR	160
Db		421 CATGTATCAAAACCAAAACCAAACTCACAGGAAGAAAGTGAAAGATTTAGAGAGAGA	480
QY		161 TYTARGALILEULIEHISGLIUEUSAPMETLYSGLIUGLIUEANPROABNTYRGLYPHEASN	180
Db		481 CATCGAAACCTCTTGATGGAATATGAAACAAACTAGAGGATCGACAGTATGTGTTTA---	537
QY		181 VALIGLUANGINSERARGILEYTCGLIUSANSERIEPROMETVALIANGIUCYSPROGIN	200
Db		538 GTGGAACAT-----GAACTCTGTGTCATTTGCMAATVGGGGCTTCCAC	582
QY		201 METPHESEPHARGVALIHISPROANGIN-----PROANLEU---	214
Db		583 CTCATATGCAATTCGGCTGATCATACGGGCAACAACCAACCACTTCCTAATCTTCAC	642
QY		215 LEUGIYLEUGIITYRGLUSERHISAPLEUSERLEU	226
Db		643 CTTGGAGATGGATTGGAGCCCATGAACTTCGCCCTT	678
RESULT 7			
ACA62518 standard; cDNA, 946 BP.			
AC	ACA62518:		
AC	ACA62518:		
DT	18-AUG-2003	(first entry)	
DE		Poplar homeotic gene PTD, cDNA.	
XX		Poplar, ss; gene; PTD; deficiens; homeotic gene; floral development;	
KM		sterile tree; pulp; paper; plant.	
XX		Populus balsamifera subsp. trichocarpa.	
XX			
XX	Key	Location/Qualifiers	
FT	CDS	1..684	
FT		/cgb= a	
FT		/product= "PTD"	
PM		/note= "This CDS is specifically claimed in claim 1"	
XX	US2003033628-A1.		
PD	13-FEB-2003.		

21-MAR-2002; 2002US-00104580.

XX 06-APR-1998; 98US-0080851P.
XX 06-APR-1999; 99US-00287700.
PR 01-OCT-1999; 99US-00410464.
XX (UWOR-) UNIV OREGON HEALTH SCI.
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX WPI; 2003-466273/44.
DR P-Psdb; ABU61893.
XX

XX New floral homeotic nucleic acid molecules, useful for the manipulation
PT of flowering in Poplar and other plant species, and for producing
PT transgenic plants having modified fertility characteristics, particularly
PT sterility.
XX
XX
XX Claim 1; Page 20-21; 48pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising at
CC least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
CC 4 homeotic genes from poplar, *PTLF* (*LEAFY* and *FLORIDA* homologue), *PTD*
CC (*DEFLICIENS* homologue), and *PTAG-1/PTAG-2* (both homologues of *AGAMOUS*).
CC Also included are a recombinant nucleic acid molecule comprising a
CC promoter sequence operably linked to the nucleic acid molecule, a cell
CC transformed with the nucleic acid molecule, a transgenic plant comprising
CC the recombinant nucleic acid molecule and the purified proteins encoded
CC by the nucleic acids. The nucleic acid molecules are useful for the
CC manipulation of flowering in Poplar and other plant species, for
CC producing transgenic plants having modified fertility characteristics
CC (particularly sterility) and in the pulp and paper industries. The
CC present sequence is the poplar *PTD* cDNA
XX
XX

Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.68e-56 Length: 946
Score: 611.00 Matches: 128
Percent Similarity: 70.69% Conservative: 36
Best Local Similarity: 55.17% Mismatches: 56
Query Match: 51.91% Indels: 12
DB: Gaps: 4

US-10-690-246A-2 (1-227) x ACA62518 (1-946)

QY 1 MetGlyArgGlyLysIleGluIleLysValIleGluAsnProThrAsnArgIleValThr 20
Db 1 ATGGGGTCGGGAAAGATTGAATCATGAAAGATGAAACCCCAACAGGCAAGTACC 60
QY 21 TyrSerLysArgArgValGlyIleLeuLysValAlaLysGluLeuThrValLeuCyAsp 40
Db 61 TACTCGAAGAGAAAGAAATGATTTTCAAGAAAGCCCAAAATCACTGATCTTGAT 120
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspLysCysSerPro 60
Db 121 GCTAAGGTCTCTTATCATGTTCTCCAACTAACAACTCAATGATGATTAAGCCC 180
QY 61 SerThrAspIleLysGlyIleTyrGlnArgTyrGlnValValThrGlyMetAspLeuTrp 80
Db 181 TCCACATTCGACAAAGAGATCTACGATCAATATCAAGACCTTAGGCAATGATCTGG 240
QY 81 AsnAlaGlnTyrGlyLysArgMetGlnAsnThrLeuLysHisLeuAsnGlnIleAsnGlnAsn 100
Db 241 GGCATCTCAATACGAGAAATGCAAGACACTTAGAGAAAGCTGATATCAATCATATAG 300
QY 101 LeuArgLysGlnIleArgArgArgLysGlyGluGluLeuGluGluMetAspIleLysGln 120
Db 301 CTGAGACAAAGAAATCAGGACAGAGAGAGAGAGGCGCTGATGATCTGAGCATTAATCAT 360
QY 121 LeuArgLysLysGluGlnThrLeuGluGlnSerLeuArgLysValAlaArgHisArgLysTyr 140
Db 361 CTGGGGGGCTTTGAGCAATATGACTGAAGCCTTGAAATGCTGCGTGGCGAGAGATAC 420

Oy		141	HISValIlealathrGlnThrAspThrTyrLysLysLeuLysSerThraArgGIuThr	160
Db		421	CATGTGATGCACAAACAGAAAAGGAAGGGTGAAAGATTTCAGAGAGAGA	480
Oy		161	TyrTrgAlaIeuIleHtIGluLeuAspMetLysGIuGIuAenProAsnTYrGLYPheAsn	180
Db		481	CATGAAACCTCTTGATGCAATTAAGAACAAAACTAAGAGATCGACAGATGGTTTA	537
Oy		181	VaIGluBengInSerArGLYerTYrGIuAnSerIleProMetVaIAeNGluCYSProGIN	200
Db		538	GTCGACAAT-----GAACTCTGTGTGACCTTGCAAATGGGGCTTCCAAc	582
Oy		201	MetHeserPheArgValAIHiSproAngIn-----ProAsnLeu---	214
Db		583	CTCATATGATTCGGCTTCATCAGGGGACACCAACCAACCACATCTCCATATCTTCAC	642
Oy		215	LeuGLYLauGLITYrGIuSerHisAspHeuSerIeu	226
Db		643	CTTGAGATGGAATTGGAGCCCATGAACCTTGCCCTT	678
RESULT 8				
AAZ57943				
ID	AAZ57943	standard; cDNA; 924 BP.		
XX AC	AAZ57943;			
XX DT	11-APR-2000	(first entry)		
XX DE	Poplar floral homeotic gene PTD cDNA.			
XX KW	Poplar; PTD; floral homeotic gene; transgenic plant; sterility; fertility; ss.			
XX OS	Populus balsamifera subsp. trichocarpa.			
XX FH	Key	Location/Qualifiers		
XX FT	CDS	1..684		
FT		/tag= a		
FT		/note= "the coding region is also specifically claimed in claim 1"		
FT		Claim 1"		
PX PN	CA2227940-A1.			
PX PD	06-OCT-1999.			
PX PF	07-APR-1998; 98CA-02227940.			
PX PR	06-APR-1998; 98US-00080851.			
PX PA	(UYOR-) UNIV OREGON HEALTH SCI.			
PX PI	Rottmann WH, Brunner AM, Sheppard LA, Straus SH;			
DR	WPI; 2000-106662/10.			
DR	P-PSDB; AAY58654.			
PT	Nucleic acid from Populus trichocarpa genes, useful for producing transgenic plants, particularly trees, with modified fertility characteristics such as sterility.			
PS	Claim 1; Page 46-47; 92pp; English.			
CC	The present sequence is that of cDNA encoding Populus balsamifera subsp. trichocarpa PTD protein (see AAY58654). The PTD gene (see AAZ57942) is 1 of 4 newly identified floral homeotic genes from this poplar species. It is a homologue of DERICENS and is expressed strongly in stamen primordia from the onset of organogenesis, and is also expressed at low levels in carpel primordia. The invention provides nucleic acid sequences of these 4 Populus genes, the corresponding cDNA sequences (see AAZ57942-49) and deduced amino acid sequences (see AAY58454-57). It also provides methods of using the gene and cDNA sequences to produce genetically engineered Populus species and other trees having modified fertility			

CC characteristic, including sterility. Genetic constructs useful in
 CC producing genetically engineered Populus and other trees include
 CC antisense versions of PTD, dominant negative mutants, and constructs
 CC useful for gene suppression. Promoter sequences may be used to obtain
 CC floral specific expression of genes such as cytochrome P450s that may be used
 CC in genetic ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Sterile trees allow increased wood
 CC yield and a reduction in the production of allergens such as pollen
 XX
 XX Sequence 924 BP, 309 A, 185 C, 201 G, 229 T, 0 U, 0 Other;

Alignment Scores:
 Pred. No.: 4,37e-54 Length: 924
 Score: 595.00 Matches: 125
 Percent Similarity: 69.83% Conservative: 37
 Best Local Similarity: 53.88% Mismatches: 58
 Query Match: 50.55% Indels: 12
 DB: 3 Gaps: 4

US-10-690-246a-2 (1-227) x AAZ57943 (1-924)

QY 1 MetGlyArgGlyIleGluIleValLeuValGluAspProThrAsnArgGlnValThr 20
 DB 1 ATGGGTCTGCAAGATTGAATCAAGAAAGATCGAAACCCCAACAGGCAAGTCACC 60
 QY 21 TyrSerIleArgArgValAlaGlyIleLeuValAlaValGluLeuThrValLeuCysAsp 40
 DB 61 TACTCGAAGAAAGAAATGGTAATTTTCAGAAAGCCCAAGAACTCACTGACTTGTGAT 120
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyIleValLeuAlaPheIleCysSerPro 60
 DB 121 GCTAAGCTCTCTTATCATCTGTCACACCTTAACCAATCAATGATGATTAAGCCCC 180
 QY 61 SerThrAspIleLeuGlyIleIleTyrGluValTyrGlnValValThrGlyMetAspLeuTyr 80
 DB 181 TCCACATCGCAAGAAAGATCTACGATCATATCAAGAACCTTGAAGCATAGATCTGTGG 240
 QY 81 AsnAlaGlnTyrGluValGlyMetGlnAsnThrLeuIleValIleLeuAsnGlnAsn 100
 DB 241 GGCATCATATACGAAATGCAAGAGACCTTGAAGCTGAATGATATCATCATATAG 300
 QY 101 LeuArgIleGluIleArgArgValGlyIleGluIleValLeuGluIleMetAspIleLeuGln 120
 DB 301 CTGAGCAAGAAATCAAGCAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
 QY 121 LeuArgIleLeuGluIleThrLeuGluIleSerLeuArgIleValAlaGlnIleArgIleTyr 140
 DB 361 CTGGCGGCTCTTGAAGCAATATGATCAAGACCTTGAATGATGCTGTGCGCAGGAACTAC 420
 QY 141 HisValIleLeuThrGlnIleThrAspThrTyrLeuValLeuValLeuValSerThrArgGluThr 160
 DB 421 CATGTGATCAAAACAAACAAACAAACCTACAGGAAGGGAAGGAAATTTAGAGAGAGAGA 480
 QY 161 TyrArgIleLeuIleHisGluLeuAspMetLeuGluIleAsnProAsnTyrGlyIlePheAsn 180
 DB 481 CATGGAACCTCTTGATGAGATATGAGCAAAATATGAGATGCAAGTATGTTTA--- 537
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
 DB 538 GTGACACAT-----GAAAGCTGCTGTGCACTTGCAATTCGAAATGGGCGCTTCAC 582
 QY 201 MetPheSerPheArgValAlaHisProAsnGln-----ProAsnLeu--- 214
 DB 583 CTCTATGCAATTCGCGCTGCATCAAGGCAACCAACCAACCAATTCCTTATCTTCAC 642
 QY 215 LeuGlyLeuGlyIleTyrGluSerHisAspLeuSerLeu 226
 DB 643 CTTCGAGATGGATTGGAGCCCATGAACTTGCGCTT 678

RESULT 9
 ADKS9650
 ID ADKS9650 standard; DNA; 637 BP.

XX

AC ADKS9650;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE plant DNA sequence which confers altered metabolic characteristic #7033.
 XX
 XX altered metabolic characteristic; plant; acid metabolism;
 XX alcohol metabolism; fatty acid metabolism;
 XX branched fatty acid metabolism; alkaloid metabolism;
 XX amino acid metabolism; ester metabolism; glyceride metabolism;
 XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;
 XX terpene metabolism; isoprenoid metabolism; alkene metabolism;
 XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
 OS Unidentified.
 PN WO2003020936-A1.
 PN 13-MAR-2003.
 PD 30-ANG-2002; 2002WO-US027884.
 PF 31-AUG-2001; 2001US-0316471P.
 PR (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX Weglarz T, Gachotte D, Blakelee B, McCreary DA, Pell RJ;
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrina I, Miller BA;
 DR WPI; 2003-313091/30.

PT Novel genes that confer altered metabolic characteristics in Nicotiana
 PT benthamiana plants, useful for altering the levels of metabolites e.g.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
 XX
 XX
 PS Claim 1; SEQ ID NO 7033; 2576bp; English.

CC The invention comprises DNA sequences which confer an altered metabolic
 CC characteristic when they are expressed in a plant. The DNA sequences of
 CC the invention are useful for producing plants with an altered metabolic
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,
 CC altered glyceride metabolism, altered phenolic metabolism, altered
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.

XX Sequence 637 BP, 155 A, 193 C, 164 G, 125 T, 0 U, 0 Other;

Alignment Scores:
 Pred. No.: 2,94e-52 Length: 637
 Score: 576.00 Matches: 107
 Percent Similarity: 84.87% Conservative: 22
 Best Local Similarity: 70.39% Mismatches: 23
 Query Match: 48.94% Indels: 0
 DB: 10 Gaps: 0

US-10-690-246a-2 (1-227) x ADKS9650 (1-637)

QY 1 MetGlyArgGlyIleGluIleValLeuValGluAspProThrAsnArgGlnValThr 20
 DB 180 ATGGGAGAGGGCAAGATTCAGATCGAAGCCGATCGAAGCCCAACAGGCGAGTGAAC 239
 QY 21 TyrSerIleArgArgValAlaGlyIleLeuValAlaValGluLeuThrValLeuCysAsp 40
 DB 240 TACTCGAAGCGCGCAAGGAGATCAAGAAAGCCCAAGAGACTCACCGTGTCTGCGAC 299

Oy		41	AlaGlnValSerLeuIleIleMetPheSerSerThrGlyValLeuAlaAspTyrCysSerPro	60
Db		300	GCCACGGTCGCATCATCATGATGTTCTCTCCACCCGGCAAGTACCAAGAGTTCTGCAGCCCT	359
Oy		61	SerThrAspIleLeuGlyValIleTyrGlnTargTyrGlnValIValThrGlyMetAspLeuTrp	80
Db		360	TCCACCGACATCAAGGGGATCTTTGACCCGCTACCGCAAGCCATCGGCACAGCCCTTGG	419
Oy		81	AsnAlaGlnTyrGlnArgMetGlnAsnThrLeuLysValLeuAsnGlnIleAsnGlnAsn	100
Db		420	ATCGACGAGTATGAGAAATATGACAGCGACGCTGAGCCATCTCAAGGACATCAACCCGAAC	479
Oy		101	LeuArgGlySerGlnIleArgArgArgTyrSerGlyGlnGluLeuGlnGlnGlyMetAspIleLysGln	120
Db		480	CTGCACCGACCGAGATACGGCAAGATGGGAAGATCTTGACGGGCTGGAGTTCCGACGAG	539
Oy		121	LeuArgGlyLeuGlnGlnThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	140
Db		540	CTGCACCGGCTTTGAGCAAAATGTCATGCGCCGCTCAAGAGAGTTGCCACAGGAAGTAT	599
Oy		141	HisValIleLeuAlaThrGlnThrAspThrTyrLysLys	152
Db		600	CATGTATCAGCACACAGACTGAACCTCAAGAA	635
RESULT 10				
ID	AAD42259		standard; cDNA; 926 BP.	
XX	AAD42259;			
AC	AAD42259;			
XX	04-NOV-2002		(first entry)	
DT				
XX				
DE	Soybean AP3 homologue cDNA from clone sfiln.pk001.116.			
XX				
KW	Floral developmental protein; flowering locus T; APETALA3; transgenic;			
KW	FT; Ap3; transgenic plant; fertility; flower development; gene mapping;			
KW	sterility; plant growth; inflorescence architecture; plant morphology;			
KW	tissue culture; cell division; soybean; gene; ss.			
XX				
OS	Glycine max.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	11..694		
FT		/*tag= a		
FT		/product= "Soybean AP3 homologue protein"		
XX				
PN	WO200244390-A2.			
XX				
PD	06-JUN-2002.			
XX				
PF	21-NOV-2001; 2001WO-US043750.			
XX				
PR	28-NOV-2000; 2000US-0253415P.			
XX				
PA	(DUPO) DU PONT DE NEMOURS & CO E I.			
PI	Cahoon EB, Cahoon RE, Klein TW, Rafalski AJ, Sakai H;			
XX				
DR	WPI; 2002-547703/58.			
XX	P-PSDB; AAE25757.			
PT	New floral developmental polypeptide having flowering locus T or Ap3			
PT	homolog activity, useful for immunological screening of cDNA expression			
XX	libraries.			
XX	Claim 6; Page 80; 88pp; English.			
XX				
CC	The present invention relates to novel floral developmental proteins,			
CC	more specifically flowering locus T (FT) or APETALA3 (AP3) homologue			
CC	proteins and polynucleotides encoding such proteins. Floral developmental			
CC	polynucleotides are useful for transforming cells or for producing plants			
CC	by transforming the plant cells with the polynucleotides and regenerating			
CC	the plants from the transformed plant cells. Sequences of the invention			

CC	are useful for immunological screening of cDNA expression libraries. The		
CC	are also useful for creating transgenic plants. Polynucleotides of the		
CC	invention are used as probes for genetically and physically mapping the		
CC	genes that they are a part of and as markers for traits linked to those		
CC	genes. AP3 homologues may be useful for engineering plant sterility or		
CC	fertility, flower development and morphology. PT or TPL1 homologues are		
CC	useful for engineering flowering time, plant growth rate, inflorescence		
CC	architecture, tissue culture morphology and rate of cell division to		
CC	enhance transformation. The present sequence is soybean AP3 homologue		
CC	cDNA		
XX			
XX	Sequence 926 BP; 304 A; 195 C; 194 G; 233 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	4,596-50	Length:	926
Score:	557.50	Matches:	109
Percent Similarity:	70.89%	Conservative:	42
Best Local Similarity:	51.17%	Mismatches:	59
Query Match:	47.37%	Indels:	3
DB:	6	Gaps:	3
US-10-690-246A-2 (1-227) x ADD42259 (1-926)			
Qy	1 MetGlyATGtGlytGleGluileuYvslleGluasnProthzAnhArglnValThr	20	
Db	11 ATGGCTAAGAGAAAGATCCAGATCAAGAGATAGAGAACACACCGCCAGGTCACT	70	
Qy	21 TYSerTLYvATgATgValglYtyleuYvslleuYvslleuYvslleuThrValleuCYvAap	40	
Db	71 TACTCTAAACGACGGAATGGCTTTCCAAAGAGCCMACAGAGTTCCGTTCTGTGGAT	130	
Qy	41 AAGlnValSerleuIllewerPheSerSerThnglYvleuAblAapTYcYsSerPro	60	
Db	131 GCCAAGGTTCTATTATATATATGTTCTCCACACCTGGAAAACCTCCACAGTACATCAGCCC	190	
Qy	61 SerThrAapIleYvsglytyleuTYrglnuATgTYrglnValValThrglYmetAepLeuTrp	80	
Db	191 TCCACCTCAACAAAGACGTTCTTCATCAATCCAGATGACTCTGGAGTTGATCTCTGG	250	
Qy	81 AenAlaGlnTYrglnuATgMetGlnAenThrleuYvslleuAenGluIleAenGlnasn	100	
Db	251 AACTCTCATTAAGAAATATGCAAGAACTTGAAAGAACTGAAGAGGTGAATAGCAAT	310	
Qy	101 LeuATgLYvsglnIleATgATgATgLYvsglytyleuGlnleuGlnuGlymetAepIleYvsgln	120	
Db	311 CTTCGTAAAGAGATTATAGCCAGAAATGGAGATGTTCTTAACGAGCTGGGCATGGAAAGAT	370	
Qy	121 LeuATgGlyLeuGlnGlnThrleuGlnGlnSerleuATgIleValArgHisATgLYvTYr	140	
Db	371 CTCAGCTCTCTGAGGAAGAAATGACAAAGCCGCCAAGTTTCTGTAGCTTAAGTAT	430	
Qy	141 HisValIleAlaThrGlnThrAapThrTYrLYvslleuYvslleuYvslleuSerThzArgGluThr	160	
Db	431 AAGGTATATAACAATCAGATTGACACCCAGAGAAAAGTTATATAAGCAAGAAAGAGTG	490	
Qy	161 TYrATgAlaLeuIleHisGlnleuAapMetLYvsglnGlnuAapProAenTYrglyPheasn	180	
Db	491 CACACAGGCTCTGTGATGATCTTGCAAAAAGCAAGAAATACAGATTGTCATTG--	540	
Qy	181 ValGlnAenGlnSerArgIleTYrglnAenSerIleProMetValAenGluCYvProGln	200	
Db	548 ATTAGAATAAGAGGGGAG--TATGATCTGTGATGGAGATTCTCAAAATTATAGGTCCAGC	600	
Qy	201 MetPheSerPheArgValAlaHisProAenGlnProasn	213	
Db	605 ATGTTGCAATTGAGC--ATACAAACCAAGCAATCTTAAGT	640	
RESULT 11			
ID	ADRO4282		
XX	ADRO4282 standard; cDNA; 926 BP.		
XX	ADRO4282;		

DT	04-NOV-2004	(first entry)
XX	Soybean Ap3 homologue encoding cDNA SEQ ID NO:49.	
DE	flowering locus T gene; FT; terminal flower; TFL; Apetala3, Ap3; plant;	
XX	floral development; plant sterility; plant fertility; flowering time;	
KW	plant growth rate; inflorescence architecture; tissue culture morphology;	
KM	cell division; Ap3 homologue; gene; ss.	
XX	Glycine max.	
OS		
XX		
FH	Key Location/Qualifiers	
FT	CDS 11..694	
FT	/tag= a	
FT	/product= "Apetala3 (Ap3) homologue"	
PN	WO2004067723-A2.	
PD	12-AUG-2004.	
XX		
PF	29-JAN-2004 ; 2004MO-US002422.	
PR	30-JAN-2003 ; 2003US-00343477.	
PA	(PION-) PIONEER HI-BRED INT INC. (DUPO) DU POINT DE NEMOURS & CO E I.	
PJ	Danilevskaya O, Hermon P, Bruggemann E, Shirboun D, Ananiev E, Rafaelert JA, Sakai H, Cahoon E, Cahoon R, Klein T,	
DR	WPI, 2004-580996/56.	
PS	P-PSTB; ADR04283.	
PT	New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3) homologues, useful for floral development, e.g. engineering plant flowering time.	
PT	Claim 6; SEQ ID NO 49; 109pp; English.	
CC	The present invention describes an isolated polynucleotide comprising a first, second, third, fourth or fifth nucleotide sequence, or their complement encoding a polypeptide either having flowering locus T gene (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also described: (1) a vector comprising the polynucleotide; (2) a recombinant DNA construct comprising the polynucleotide; (3) transforming a cell by transforming a cell with the polynucleotide; (4) a cell comprising the recombinant DNA construct; (5) producing a plant comprising transforming a plant cell with the polynucleotide, and regenerating a plant from the transformed plant cell; (6) a plant comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (8) an isolated polynucleotide comprising a first nucleotide sequence, where the first nucleotide sequence contains at least 30 nucleotides, and where the first nucleotide sequence is comprised by another polynucleotide, where the other polynucleotide includes the second, third, fourth, fifth or sixth nucleotide sequence; (9) an isolated polypeptide having FT or Ap3 homologue activity, as described above; and (10) isolating a polypeptide encoded by the polynucleotide comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide operably linked to a regulatory sequence. The polynucleotides are useful for floral development, e.g. engineering plant sterility/fertility, flowering time, plant growth rate, inflorescence architecture, and tissue culture morphology and the rate of cell division to enhance transformation. The present sequence encodes an Ap3 homologue from the present invention.	
CC		
XX		
SEQ	Sequence 926 BP; 304 A; 195 C; 194 G; 233 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	4,59e-50	length: 926
Score:	557.50	Matches: 109
Percent Similarity:	70.8%	Conservative: 42
Best Local Similarity:	51.1%	Mismatches: 59

Query Match:	47.37%	Indel:	3
DB:	13	Gaps:	3
US-10-690-246A-2 (1-227) × ADR04282 (1-926)			
QY	1 MetGlyArgGlyValIleGluIleuValuyluValuIleGluIleuProThrAsnArgGlnValThr		20
DB	11 ATGGCTAGAGAAAGATCCAGATCAAGAGATAGAAACAACCAACCGCAGATCACT		70
QY	21 TyrSerIleArgArgValGlyIleuValuyluValuIleGluIleuThrValIleuCysAsp		40
DB	71 TACTCTAAACGAGGATGGCTTTTCAAGAAAGCCCAACGAGCTTACCGTCTCTGGCAT		130
QY	41 AlAGlnValSerIleuIleuMetPheSerSerThrGlyValuValuIleAspTyrCysSerPro		60
DB	131 GCCAAGGATTTCTATTTATTTATGTTCTCCAGACTGGAAATCTCCAGCTAATCAACGCC		190
QY	61 SerThrAspIleIleuGlyIleTyrGluArgTyrGlnValValThrGlyMetAspIleuTyr		80
DB	191 TCCACCTCAACAAAGAGATGTTCTTCATCAATTCAGAGATGACTGGGAGTTCCTCGG		250
QY	81 AsnAlaGlnTyrGluArgMetGlnAsnThrIleuValuyluValuIleAsnGlnIleAsnGln		100
DB	251 AACTCTATTACGAGATATGCAAGAACTTGAAGAACTGAAAGAGGTGATATGGAT		310
QY	101 LeuArgIleGluIleArgArgArgValuGluIleuGluIleuGluIleuMetAspIleuGln		120
DB	311 CTTCGTAAAGAGATTGGCAGAGATGGAGATTGCTGAAACGAGCTGGGCAATGAGAT		370
QY	121 LeuArgIleuGluIleuThrIleuGluIleuGluIleuValIleValArgIleuTyr		140
DB	371 CTCAGACTCTTTAGAGAAAGATGCAAGAGCGCGCCAGCTTGTTCGAGACGTATGAT		430
QY	141 HisValIleAlaThrGlnThrAspThrTyrIleValuyluValuIleuSerThrArgGluThr		160
DB	431 AAGGTGATTAACAAATCAGATTGACACCCAGAGAAAGTTTAATTAAGAAAGAAAGTG		490
QY	161 TyrArgAlaIleuIleuIleuGluLeuAspMetIleuGluIleuProAsnTyrGlyPheAsn		180
DB	491 CACAAAGGCTCTCGATGACTTGGATGCAAAAGCAAGAAATCCAGTTTGCAATTG--		547
QY	181 ValIleuGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysAspGln		200
DB	548 ATATATTAATGAGAGGAG--TTTAGTCTGTGATCGCATTTCTCAATTATAGTCCAGCC		600
QY	201 MetPheSerPheArgValValHisProAsnGlnProAsn 213		
DB	605 ATGTTGCAATTGAGC--ATACAAACCAAGCATTCTTCAAT 640		
RESULT 12			
ACNS3850			
ID	ACNS3850 standard; cDNA; 644 BP.		
AC			
ACNS3850;			
XX	02-DEC-2004 (first entry)		
XX			
XX	Cotton androecium tissue EST Clone ID: LIB3828-013-Q1-K6-F12, SEQ.8631.		
XX			
XX	Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium		
KW	variety Ncotton338; library LIB3828; molecular tag; molecular marker:		
KW	genetic mapping; molecular mapping; seed germination; plant growth;		
XX	plant quality; plant yield; plant breeding; tissue printing; ss.		
XX			
OS	Gossypium hirsutum.		
XX			
XX	US2004123340-A1.		
XX			
XX	24-JUN-2004.		
XX			
XX	12-DEC-2001; 2001US-00021323.		
XX			
XX	14-DEC-2000; 2000US-0255619P.		

XX (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 PI Deikman J, Peng PCC, Fincher KL, Ziegler TE;
 DR WPI; 2004-479808/45.
 XX
 PT New isolated nucleic acid molecule that encodes a plant protein or its
 PT fragment, useful for isolating a variety of agronomically significant
 PT genes associated with plant growth, quality or yield, and as molecular
 PT tags to map genes.
 XX
 PS Claim 1; SEQ ID NO 8631; 34pp; English.
 XX
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
 CC from primed or non-primed seeds from variety DP50B, mature seeds from
 CC variety Coker 312 Bowers 11 96 Field, and androecium tissue, gynoecium
 CC tissue, developing fibres, carpel walls and septa from variety
 CC Nucletron33B. The invention also relates to substantially purified
 CC proteins or their fragments encoded by nucleic acid molecules of the
 CC invention, and to transformed plants having a nucleic acid construct
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
 CC molecular tags to isolate genetic regions, to isolate genes, to map
 CC genes, to determine gene function and to determine whether genes are
 CC members of a particular gene family. The nucleic acid molecules may be
 CC used for isolating a variety of agronomically significant genes
 CC associated with plant growth, quality, yield, and could also serve as
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are
 CC also useful for identifying genes important in initiating and maintaining
 CC seed germination or that may be used to mitigate stresses encountered
 CC during seed germination. The ESTs additionally enable the acquisition of
 CC promoters and cis-regulatory elements which will be useful to express
 CC agronomically significant genes in these tissues and/or other tissues,
 CC and also permits the acquisition of molecular markers useful in breeding
 CC schemes, genetic and molecular mapping, and in cloning of agronomically
 CC significant genes. The nucleic acid molecules are further useful for
 CC detecting the expression level or pattern of a protein or mRNA and for
 CC detecting the presence or quantity of a protein by tissue printing. The
 CC present sequence represents a specifically claimed EST isolated from a
 CC cotton variety Nucletron33B androecium tissue cDNA library (LIB3828). The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the US
 CC Patent Office at seqdata.uspto.gov/sequence.html?docID=US20040123340
 CC
 XX
 SQ Sequence 644 BP; 214 A; 120 C; 150 G; 158 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 3,699-47 Length: 644
 Score: 528.50 Matches: 108
 Percent Similarity: 71.84% Conservative: 40
 Best Local Similarity: 52.43% Mismatches: 56
 Query Match: 44.90% Indels: 3
 Gaps: 2
 US-10-690-246a-2 (1-227) x ACN53850 (1-644)
 QY 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgGlnValThr 20
 DB 32 ATGGCTCAGGAGGAGATCAAGATCAAGTGAAGAACTGACCAACAGGCAAGTCAAG 91
 QY 21 TyrSerLysArgValGlyIleLeuLysValAlaLysGluLeuThrValLeuGlyAsp 40
 DB 92 TATTCGAAGAGAAAGACGGCTCTTTCAGAAAGCTAATGAACTTACAGTTCTTGGCAT 151
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
 DB 152 GCTAAGGTTTCATCATGATGTTTTCACCTACTGTTAACTCCATGACGATTTACGCCCT 211
 QY 61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80

DB 212 TCACCAACAGCAAGAGCAAGTAATTCATCTACGTAACGAGAAACCTGGGATCGCATATCTCG 271
 QY 81 AsnAlaGlnTyrGlyLysArgGlnLeuThrLeuLysGlnIleLeuAsnGlnIleAsnGlnIle 100
 DB 272 AACCCACCTATGAGAAATGCAAGACGACGTTGAGCACTGAAAGAGGTTTAAACAGAAC 331
 QY 101 LeuArgLysGluIleLeuArgArgLysGlyGluIleLeuGluGlyMetAspIleLysGln 120
 DB 332 CTGCGCAAGAGAGATTGAGAGAGATGGCGCACTGTTTAAATGATTGACATCGAAAGAT 391
 QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
 DB 392 CTGGGCTTTCGAAACAAAGAAATGAGAGACTCTGTCACTTATTCGTATTAAGATAT 451
 QY 141 HisValIleLeuThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
 DB 452 CGTGTCTCTCCAAACGATCGATCTTCACAGAAAGAGTGAATGTGAAAGATGA 511
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGlnAspProAsnTyrGlyPheAsn 180
 DB 512 CACAAAATCTCTTACATGAACTGGAATCCCTGAAAGAAAGATCA--TATGGAATTA-- 566
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
 DB 567 GTTGATTAATGAGAGGAGAT--TATGATACCCGATCGGATTCGAAATGAGAGCTCTCGT 623
 QY 201 MetPheSerPheArgVal 206
 DB 624 ATATTTGCTTACGCCCTG 641
 RESULT 13
 AA051189 ID AA051189 standard; DNA; 882 BP.
 AC AA051189;
 XT 25-MAR-2003 (revised)
 DT 19-JUN-1994 (first entry)
 XX Homeotic gene green petal.
 DE Plant; organ morphogenesis; control; petunia; petals; se.
 XX Petunia.
 OS
 XX Key Location/Qualifiers
 FT CDS 17..713
 FT /*tag= a
 PN MO9321322-A1.
 XX 28-OCT-1993.
 PD 13-APR-1993; 93WO-US003508.
 PE 13-APR-1992; 92US-00867580.
 PR 06-JUL-1992; 92US-00909589.
 XX (UTRQ) UNIV ROCKEFELLER.
 PA Halfter U, Van Der Krol AR, Kush A, Chua N;
 PI WPI; 1993-351732/44.
 DR P-PSDB; AAR43385.
 XX Plant organ morphogenesis control and determ. - by regulating the
 PT expression of homeotic genes which determine the identity of the organ.
 XX Claim 13; Fig 2; 74pp; English.
 CC The homeotic gene green petal from petunia has been cloned and
 CC characterised previously. The gene was used in a new method for

CC controlling the morphogenesis of plant organs comprising regulating the
 CC expression of the gene using ectopic expression. Such a method can be
 CC used to determine and control plant organ morphogenesis, such as
 CC modifying petals without altering the reproductive portions of the
 CC flower. See also AA051190-1. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 882 BP; 306 A; 155 C; 182 G; 239 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	882
Score:	528.00	Matches: 105
Percent Similarity:	69.30%	Conservative: 44
Best Local Similarity:	48.84%	Mismatches: 60
Query Match:	44.86%	Indels: 6
DB:	2	Gaps: 3

US-10-690-246A-2 (1-227) x AA051189 (1-882)

QY 1 MetGlyArgGlyValIleGluIleValIleGluAsnProThrAsnArgIValThr 20
 DB 18 ATGGCTGCGGAAAGATCCAGATCAAGATGAAACCAACCAAGGCAAGTGACA 77
 QY 21 TyserylAsnArgValGlyIleLeuValAlaIleGluLeuThrValIleuCyAsp 40
 DB 78 TATTTAAGAGAAAGAAATGAGACTTTCAAGAGGCTTAATGACTCACTGTTTGTGAT 137
 QY 41 AlGlnValSerIleuIleMetPheSerSerThGlyValLeuAlaAspIleCySerPro 60
 DB 138 GCCAAGTTCCCAATATGATGATTCAGACTGGCAAGCTTCATGATTCATTAGCCCA 197
 QY 61 SerThrAspIleValGlyIleValGlyValGlyValIleValIleValIleValIleVal 80
 DB 198 TCTATACGACCTAAGCAGTTGCTGATCTGATCCAAAGCCTGTTGAGATGATCTTTGG 257
 QY 81 AsnAlGlnIleValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100
 DB 258 AACTCCCATATGAGAAATGAGCAAGAGCACTGAGGAAGCTTAAGAAAGTAATGAGAAAT 317
 QY 101 LeuArgIleGluIleValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 120
 DB 318 CTCGGAAGAGATCAAGGAGAGATGGGAAAGCCTTAACGATCGAATGATGAGCAG 377
 QY 121 LeuArgGlyIleuGluIleValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140
 DB 378 TTGGAAGAGCTCAATGGAAGATGTCGACATTTCTCAAGCTTATCTGAAAGAACTAT 437
 QY 141 HisValIleAlaThrGlnThrAspThrIleValIleValIleValIleValIleValIleValIle 160
 DB 438 AAGGTGATTCGCAATGATGATGAGACATTCAGAGAAAGCTCAAGAAATGAGAAAT 497
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleAsnProAsnIleGlyPheAsn 180
 DB 498 CATTAGGATCTCTGCTTGAATTTGAGCAACCAAGCAACCA-----TATGGG 548
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValIleGluIleCySerGln 200
 DB 549 CTAGTTGAACAGAGAGTGAATCTGATCTGCTGCTTTTCCAAATGAGAGGAGCATCGC 608
 QY 201 MetPheSerPheArgValIleHisProAsn-----GlnProAsn 213
 DB 609 ATATTAGCTTTAGC---CTTCAACCAACCAACCAACCAACCAAT 650
 RESULT 14
 ID AAS00104 standard; cDNA; 982 BP.
 XX AAS00104;
 AC XX
 DT 11-SEP-2003 (revised)
 DT 17-MAY-2001 (first entry)
 XX
 DE Granny Smith apple cDNA encoding MdAP3.

XX Granny Smith apple; MdAP3; seedless fruit; horticulture;
 KW accelerated breeding programme; cross pollination; transgenic plant;
 KW biennial bearing tendency; coding moth; ss.
 OS Malus x domestica; var. Granny Smith.

XX Key Location/Qualifiers
 FT 1..699
 FT CDS /tag= a
 FT /product= "MdAP3"

XX MO200117334-A1.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000MO-NZ000176.

XX 07-SEP-1999; 99NZ-00337688.

XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.

XX Yao J, Morris BA;

XX MPI; 2001-235145/24.

XX P-PSDB; AAU00187.

PT New genetically modified fruiting plants that does not functionally
 PT express MdPI or MdAP3 peptides, useful for producing seedless fruits,
 PT specifically apple and its related species.

XX Claim 17; Fig 6; 41pp; English.

XX The sequence encodes Granny Smith apple MdAP3. The invention concerns a
 CC fruiting plant that has been genetically modified so that it does not
 CC functionally express the MdPI or MdAP3 peptide, producing seedless
 CC fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
 CC may be used to transform fruiting plants, specifically apple and pear.
 CC The polynucleotides may be used in modulating, reducing or eliminating
 CC seed-bearing capacity in fruiting plants, used in horticulture, and in
 CC breeding programmes to monitor the progress in breeding a stable seedless
 CC fruiting plant. The polynucleotides may also be used in programmes for
 CC identifying nucleic acid variants from fruiting plants. They can be used
 CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 CC for use in an accelerated breeding programme to produce seedless fruit.
 CC They may also be used in designing probes and primers for MdPI or MdAP3,
 CC or their variants. The seedless fruiting plant is more convenient than
 CC seeded fruit since these can be cropped without pollination, reducing
 CC dependence on bees, pollinator varieties and warm weather at flowering.
 CC The absence of pollen is also advantageous to alleviate environmental
 CC concerns regarding the transfer of transgenes to non-transgenic
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
 CC tendencies that have been attributed to the inhibition of flower bud
 CC formation by developing seeds and are less susceptible to codling moth
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 CC field)

XX Sequence 982 BP; 308 A; 203 C; 226 G; 245 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	982
Score:	1.04e-46	Matches: 112
Percent Similarity:	526.50	Conservative: 39
Best Local Similarity:	63.45%	Mismatches: 70
Query Match:	47.06%	Indels: 17
DB:	4	Gaps: 4

US-10-690-246A-2 (1-227) x AAS00104 (1-982)

QY 1 MetGlyArgGlyValIleGluIleValIleGluAsnProThrAsnArgIValThr 20
 DB 1 ATGGCGCGGGAAGTGAATCAAGTGAATGAAACCAAGCAAGGCAAGTGAC 60


```

Db      514 CATGAAATCTCTTGGCTTGATTGATGCAAGACAGAGGACCA-----TATCGA 564
QY      181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
Db      565 TTGGTTGAGCAGAGAGGAGACTATACTCTGTGCTTGATTCCCAATGGAGGAGCCACGC 624
QY      201 Met 201
Db      625 ATA 627

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Search completed: October 6, 2005, 13:09:50
 Job time : 568 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 6, 2005, 12:43:06 ; Search time 3342 Seconds
(without alignments)
2585.455 million cell updates/sec

Title: US-10-690-246a-2

Perfect score: 1177

Sequence: 1 MGRGKIKIKIENPTNRQVT.....HPNQPLIGIKYSHLSLA 227

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q/cgr2_1/USPTO.spool/US10690246/runat 05102005 110910 6447/app query.fasta_1.391
-DB=EST -QPM=faabap -SUPFI=p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USPR=US10690246 @CGN 1.1 3437 @runat 05102005 110910 6447 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUOTRY -NEG_SCORES=0 -WAIT -DSBLOC=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	57.3	872	6	CD439730 EL01N0528
2	675	57.3	1273	3	AY109302 Zea mays
3	621	52.8	694	6	CB921382 VVD070D08
4	618	52.5	585	6	CB626851 OS11B01G
5	588	50.0	645	6	BE497689 WHE955.D0
6	587.5	49.9	710	5	BU875031 V001F01.P
7	578	49.1	651	5	BU994760 HM08C02r
8	576	48.9	615	7	CO997489 11u01-6ms
9	573	48.7	762	6	CB971393 CAB10005_

10	570.5	48.5	639	5	BU879075	BU879075 V055E10.P
11	569	48.3	698	2	AM737915	AM737915 EST339342
12	561	47.7	605	5	BU877396	BU877396 V033R07.P
13	557	47.3	605	6	CA732396	CA732396 w1p1c.pk0
14	556.5	47.3	692	6	CB972246	CB972246 CAB10006_
15	555.5	47.2	591	7	CO995351	CO995351 eca01-5c8
16	553.5	47.0	650	7	CV005022	CV005022 eca01-13c
17	550	46.7	721	1	AJ784752	AJ784752 AJ784752
18	549	46.6	652	4	BI924444	BI924444 EST544333
19	548	46.6	691	7	CO109959	CO109959 GR_EB004
20	547	46.5	605	6	CA597172	CA597172 wpa1c.pk0
21	538	45.7	532	2	BF291839	BF291839 WHE2204_E
22	536	45.5	630	6	CA600487	CA600487 waw1c.pk0
23	534	45.4	508	5	BU878141	BU878141 V043F04.P
24	534	45.4	757	1	AJ568207	AJ568207 AJ568207
25	533	45.3	697	1	AJ568191	AJ568191 AJ568191
26	533	45.3	722	1	AJ559554	AJ559554 AJ559554
27	533	45.3	762	1	AJ799190	AJ799190 AJ799190
28	533	45.3	784	1	AJ790416	AJ790416 AJ790416
29	524	44.5	689	7	CO106481	CO106481 GR_EB003
30	523	44.4	800	1	AJ568199	AJ568199 AJ568199
31	522	44.4	724	7	CO123447	CO123447 GR_EB051
32	521.5	44.3	868	7	CV505838	CV505838 72490.1.M
33	521	44.3	581	5	BU880121	BU880121 UN41FP12
34	515.5	43.8	717	6	CD838295	CD838295 RF02.110K
35	514.5	43.7	660	7	CV516063	CV516063 0048P0012
36	514.5	43.7	661	7	CV516051	CV516051 0048P0012
37	514	43.7	666	7	CV516589	CV516589 0048P0015
38	514	43.7	682	7	CV515313	CV515313 0048P0008
39	511	43.4	616	2	BF324502	BF324502 eu12902.Y
40	511	43.4	623	1	AJ801659	AJ801659 AJ801659
41	508.5	43.2	871	3	CN80A722	CN80A722 ARB01d0p8
42	507	43.1	714	4	BI929568	BI929568 EST549457
43	506.5	43.0	624	7	CK118415	CK118415 217b1.P1
44	506.5	43.0	704	7	CV295468	CV295468 EST883845
45	506.5	43.0	969	3	CNS09YEQ	XB842104 Arabidops

ALIGNMENTS

RESULT 1
LOCUS CD439730 872 bp mRNA linear EST 03-JUN-2003
DEFINITION EL01N0528D01.b Endosperm_5 Zea mays cDNA, mRNA sequence.
ACCESSION CD439730
VERSION CD439730.1 GI:31355373
KEYWORDS
SOURCE
ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 872)
Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F.,
Larkins,B., Becraft,P. and Messing,J.
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)

JOURNAL
COMMENT Contact: Lai, Jinseng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu

Seq primer: T3.
Location/Qualifiers
1..872
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"

FEATURES
Source

[illegible]

DB:	6	Gaps:	4
US-10-690-246A-2 (1-227) × CB921382 (1-694)			
QY	2	GLYARGSLYSLIEGLIULIULYSLSIIIEGLIUSNProThraSNrGLIValIThrTYR	21
Db	1	GGTGTGGGAAGATTGATCAAGAGGATGAGAACCCCAACAGGCGGTCACTAC	60
QY	22	SErLYeARgARgALgIYLIELeULySLyALILySGILuLeuThrValLeuCYeASpALA	41
Db	61	TCCAAAGGAGAAATGGTATTTTCAAGAAAGCCAGAGCTCACCTTTTGTGATGT	120
QY	42	GLIValSerLeuIleMetPheSerSerThGlyLysLeuAlaSPryCYeSerProSer	61
Db	121	AAGGTTTCACTCATCTTTCTCCAAATCTGGAAATTCACGAATATACAGTCTACT	180
QY	62	ThraSPILeULySLyIeTYrgIuARgTYrGLIValValThrGLyMetAspLeuTPAsn	81
Db	181	ATACGACGAAAAAGGCTACGATCAAGTATCAGAAAGCTTAGGGATTGATCTTTGGAGC	240
QY	82	AlaGLINTYrGLUArgMetGLInaenThrLeuLysIleuAnGLIleASnGLInaLeu	101
Db	241	TCTCATACGACGAAATGCAAGAAACCTTCGAAATCTGAAGAGATCAACAAATTA	300
QY	102	ArgLYeGLIULIeARgARgSLySLYGLIUGLUeUGLUeGLyMetAspIleLYeSGLIneu	121
Db	301	AGGAGAGAGATCAAGCAAGATGGGTAAGATTGGCCGATCTGACCATTTGAGAGACTG	360
QY	122	ArgSLyLeuGLInGLInThrLeuGLIUGLUeSerLeuARgIleValARgHISARgLYeTYrHIS	141
Db	361	CGCGGCTTGAAGCAAGATGAGAGCGTCTTTAGATTAGTACGCAAGCAAGTACAC	420
QY	142	ValIleAlaThrGLInThrAspThrTYrLYeLYeLYeLYeLYeLYeSerThrARgGLIThrTYr	161
Db	421	GTGATTCAAACTCAGACCGAGACTTACAGGAAAGGTCAAGAACTTGAAGAAACAAC	480
QY	162	ArgALeULeULeHISGLIULeUSpMetLYeSGLIUGLUeSNProAsnTYrGLYPhEASnVal	181
Db	481	GGAATCTCTCTTCAACTTGGAGCAAAATGCATGATCCACTTACGATTACGATTAC	537
QY	182	GLIUSnGLInSerARgIleTYrGLIUSnSerIleProMetValASnGLIYsProGLInMet	201
Db	538	GAAATATATGAGAT---TATGAATCAGCGGTGCATTCGCAACGGGGCTTCCAACTC	594
QY	202	PheSerPheARgValValHISProASnGLInProASnLeu---LeuSGLyLeuGLIYrGLIu	220
Db	595	TATGCTTTCCG---CTGCAATCAGGCCCACTTATCTTCAACATGATGGGGATATGGA	651
QY	221	SErHISAspLeuSerLeuAla 227	
Db	652	TCACATGATCTGCGCTTGCT 672	
RESULT 4			
LOCUS	CB626851	585 bp	mRNA linear EST 08-APR-2003
DEFINITION	OSITIEB01G03.f OSITIEB Oryza sativa (indica cultivar-group) cDNA		
ACCESSION	CB626851		
VERSION	CB626851.1	GI:29621840	
KEYWORDS	EST.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group)		
REFERENCE	Jantaanurayar,C., Lu,G., Gowda,M., Hatfield,D., Zhou,B., Mazur,E.,G.		
AUTHORS	Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.		
TITLE	Large-scale identification of ESTs involved in the interaction		
JOURNAL	between rice and Magnaporthe oryzae		
COMMENT	Unpublished (2003)		
	Contact: Rod Wing		
	Arizona Genomics Institute		

University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3867
 Fax: 520 621 9288
 Email: <http://genome.arizona.edu>
 PCR primers
 FORWARD: gta aac cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 plate: 01 row: G column: 03
 Seq primer: gta aac cga cgg cca gtc.

FEATURES

source
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 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="IR36"
 /db_xref="taxon:39946"
 /clone="OSIIB01G03"
 /issue_type="Leaf"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_lib="OSIIBb"
 /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

ORIGIN

Alignment Scores:

Pred. No.: 5.53e-63 Length: 585
 Score: 618.00 Matches: 116
 Percent Similarity: 82.66% Conservative: 27
 Best Local Similarity: 67.05% Mismatches: 30
 Query Match: 52.51% Indels: 0
 DB: 6 Gaps: 0

US-10-690-246a-2 (1-227) x CB626851 (1-585)

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QY      1 MetG1AAGG1ylysi1leg1uilelyy1leg1uanspProthrAsnArgInValThr 20
DB      30 ATGGGGAGGGGCAAGATCGAGATCGAGCGATCGAGAACCGACCAAGCGAGGTGAC 89
QY      21 TyrSerLyAARGArGValGyl1leuLybLybAlaLybGluLeuThrValLeuCybAaP 40
DB      90 TACTCGAAGGCGCGCACGGGGATCATGAAAGGCCACCGGCTCACCGCTCTCGAC 149
QY      41 AlaG1ValSerLeuilemetPheSerSerThG1ylybLeuAlaApTyryCybSerPro 60
DB      150 GCCCAGGTGCCATCATCATCTCTCTCTCCACCGGCAAGTACCAAGATTCTGACGCTT 209
QY      61 SerThAsp1lelysg1y1etyrg1uArgTyrg1nValValThrGlyMetAapLeuTrp 80
DB      210 TCCACCGACATCAAGGGGATCTTTGACCGCTTACAGCAAGCCATCGGACCAAGCTTTGG 269
QY      81 AsnAlaG1nTyrg1uArgMetG1nAsnThrLeuLybH1leuAnsG1uileAnsG1nAsn 100
DB      270 ATCGAGCAGATATAGATATATGACAGCGCACGCTGATTCAGAGCATCAACCGCAC 329
QY      101 LeuArgLybG1uileArgArGArGlybG1yG1uLeuLeuG1uileMetAap1lelybG1n 120
DB      330 CTGCGCACCGAGATCCAGGCAAGAGATGGGAAAGATCTGAGCGGCTGGAGTTGACAGAG 389
QY      121 LeuArgG1yLeuG1uInThrLeuG1uG1uSerLeuArg1leValArgH1sArgLybTy 140
DB      390 CTGCGGGCTTTAGAGCAAAATGTCGATGCCGCTCAAGAGAGGTGCGCCACAGAGATAT 449
QY      141 HisVal1leAlaThrG1nThrAspThrTyryLybLybLeuLybSerThrArgG1uThr 160
DB      450 CATGTATACGACACACAGACTGAACCTTACAGAAAGAGTGAAGCACTCTCTACGAGCGG 509
QY      161 TyrArgAlaLeu1leHisG1uLeuAapMetLybG1uG1u 173
DB      510 TACAGACTCTGACAGAGAGCTGGGGGTGTGGCAGAG 548

```

RESULT 5

BE497689
 LOCUS BE497689 645 bp mRNA linear EST 04-AUG-2000
 DEFINITION WHB955_D02_G03ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHB955_D02_G03, mRNA sequence.

ACCESSION BE497689
 VERSION BE497689.1 GI:9696306
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 645)

AUTHORS

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hela, C.C., Kang, Y., Lazo, G.R., Miller, R., Rauech, C.J., Seaton, C.L. and Tong, J.C.

TITLE

The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773
 Fax: 5105959818

Email: canderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1..645

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHB955_D02_G03"

/issue_type="Spike Before anthesis"

/dev_stage="Adult plant"

/lab_host="E. coli S04R"

/clone_lib="Wheat pre-anthesis spike cDNA library"

/note="Vector: lambda uni-ZAP XR, excised phagmid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagmids in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Alignment Scores:

Pred. No.: 2.37e-59 Length: 645
 Score: 588.00 Matches: 116
 Percent Similarity: 79.23% Conservative: 29
 Best Local Similarity: 63.39% Mismatches: 34
 Query Match: 49.96% Indels: 4
 DB: 2 Gaps: 3

US-10-690-246a-2 (1-227) x BE497689 (1-645)

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QY      1 MetG1AARG1ylysi1leg1uilelyy1leg1uanspProthrAsnArgInValThr 20
DB      108 ATGGGGCGGGGGAAGATCGAATTAAGCGGATCGAGAACCGCAACAGCGAGGTGACC 167
QY      21 TyrSerLyAARGArGValGyl1leuLybLybAlaLybGluLeuThrValLeuCybAaP 40
DB      168 TACTCGAAGGCGCGGCTGGGATCATGAGAAAGCGCGGAGACTCAGTGTCTGCGAGC 227
QY      41 AlaG1nValSerLeuilemetPheSerSerThG1ylybLeuAlaApTyryCybSerPro 60
DB      228 GCCCAGGTGCCATCATCTCTCTCTCCACCGGCAAGTACCAAGATTCTGACGACCC 287

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Qy 61 SerThrAspIleLeuGlyIleTyrGlnValArgTyrGlnValValThrGlyMetAspLeuTyr 80
 Db 288 GGACCGACATCAAGGGATCTTTGACCGCTACACAGCGCATCGGACCAAGCTGTGG 347
 Qy 81 AsnAlaGlnTyrGlnUargMetGlnAsnThrLeuValHisIleuAsnGlnIleAsnGlnAsn 100
 Db 348 ATGACGACATGATAGATATGACGCGCATGAGCCATCTCAAGACATCAATCGGAC 407
 Qy 101 LeuArgLyseGlnIleArgArgTyrGlyGlnIleuGlnIleMetAspIleLeuGln 120
 Db 408 CTCGCGACCGAGATC-----AGATGGGTGAAGATCTGACCGCTCGAGATCGAGAG 461
 Qy 121 LeuArgGlyLeuGlnIleThrLeuGlnIleuGlnIleuArgIleValArgHisArgGlyTyr 140
 Db 462 CTCGCGACCTTGAGCAAAATGTCAGTCGCTCTCAAGAGGTTCCGACAGAGATAT 521
 Qy 141 HisValIleAlaThrGlnThrAspThrTyrTyrValLeuValLeuValSerThrArgGluThr 160
 Db 522 CATGTGATCAACAGCGAGCTGAAACCTACAGAGAGGTGAAGCATCTCCAGAGAGCA 581
 Qy 161 TyrArgAlaLeuIleHisGlnLeuAspMetLeuGlnIleuAsnProAsnTyrGlyPheAsn 180
 Db 582 TACAGAAATCTGCAGCAGAGCTGGTATGCGCAGAGAC---CCGGCTACGGTTT--- 635
 Qy 181 ValGluAsn 183
 Db 636 GTGGACAC 644

RESULT 6
 BU875031 710 bp mRNA linear EST 16-OCT-2002
 LOCUS V001F01 Populus flower cDNA library Populus balsamifera subsp.
 DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION BU875031.1 GI:24066555
 VERSION BU875031.1
 KEYWORDS EST.
 SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
 ORGANISM Populus balsamifera subsp. trichocarpa

REFERENCE 1 (bases 1 to 710)
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL Unpublished (2002)
 COMMENT Contact: BHADERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
 source Location/Qualifier
 1..710
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
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 /clone_lib="Populus flower cDNA library"
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ORIGIN
 Alignment Scores:
 Pred. No.: 3,1e-59 Length: 710
 Score: 587.50 Matches: 121
 Percent Similarity: 69.37% Conservative: 33
 Best Local Similarity: 54.50% Mismatches: 53
 Query Match: 49.92% Indels: 15
 DB: 5 Gaps: 3

US-10-690-246a-2 (1-227) x BU875031 (1-710)

Qy 1 MetGlyArgGlyValIleGluValIleValSerProThrAsnArgIleValThr 20
 Db 85 ATGGGTCTGTGAAGATGTAATCAAGAGATCGAAGAACCCAGAGAGAGAGAGAG 144
 Qy 21 TyrSerLeuArgArgValIleGlyIleLeuValIleValSerProThrValIleuCyAsp 40
 Db 145 TACTCAGAGAGAGAGATGTAATTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 204
 Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
 Db 205 GCTAAGTCTCTTATCATGTTCTTCAACATCAACAACTCAATGATGATTAACCCC 264
 Qy 61 SerThrAspIleLeuGlyIleTyrGlnValArgTyrGlnValValThrGlyMetAspLeuTyr 80
 Db 265 TTCACATTCAGCAAGAGAGATCTACATGATCAATATCAAGAGCTTTAGGCAATGTCGTGG 324
 Qy 81 AsnAlaGlnTyrGlnUargMetGlnAsnThrLeuValHisIleuAsnGlnIleAsnGlnAsn 100
 Db 325 GGACCTCAATACAGAGAAATGCAAGAGCATTCAGAGAGAGAGAGAGAGAGAGAGAG 384
 Qy 101 LeuArgLyseGlnIleArgArgTyrGlyGlnIleuGlnIleuMetAspIleLeuGln 120
 Db 385 CTGAGACAGAAATCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 444
 Qy 121 LeuArgGlyLeuGlnIleThrLeuGlnIleuGlnIleuArgIleValArgHisArgGlyTyr 140
 Db 445 CTCGCGGCTTTAGAGCAACATGATGATGAGAGCTTGAATGTGTGCGTGCAGAGAGATC 504
 Qy 141 HisValIleAlaThrGlnThrAspThrTyrTyrValLeuValLeuValSerThrArgGluThr 160
 Db 505 CATGTATCAAAACACAAACGAAACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 564
 Qy 161 TyrArgAlaLeuIleHisGlnLeuAspMetLeuGlnIleuAsnProAsnTyrGlyPheAsn 180
 Db 565 CATGAAACCTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 621
 Qy 181 ValGluAsnGlnSerArgIleTyrGlnAsnSerIleProMetValIleGlnTyrProGln 200
 Db 622 GTGACAAAT-----GAAGCTGCTGTTGCAATTCGAATGAGGCTTCAC 666
 Qy 201 MetPheSerThrArgValIleHisProAsnGlnProAsnLeuGlyLeuGlyTyrGlu 220
 Db 667 CTTATGCAATTCGCTGATC-----GGGACAC 699
 Qy 221 SerHis 222
 Db 700 CACCAAC 705

RESULT 7
 BU994760 651 bp mRNA linear EST 23-OCT-2002
 LOCUS HM08C02r HM Hordeum vulgare subsp. vulgare cDNA clone HM08C02
 DEFINITION S-PRIME, mRNA sequence.

ACCESSION BU994760.1 GI:24271743
 VERSION BU994760
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE 1 (bases 1 to 651)
 Zhang, H., Meschke, W., Michalek, W., Stein, N. and Graner, A.
 EST sequencing and analysis in barley (2002)

JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595

Email: stein@pk-gatersleben.de
Insert Length: 651 Std Error: 0.00
Plate: 8 row: C column: 2
Seq primer: M13rev.
Location/Qualifiers

FEATURES

source

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1..651
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:254578"
/db_xref="taxon:112509"
/clone="HM08C02"
/issue_type="male inflorescences"
/dev_stage="male inflorescences (approx. 2 mm in size), green anther stage"
/lab_host="X110-Gold"
/clone_lib="PM"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

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ORIGIN

Alignment Scores:

Pred. No.: 3,73e-58 Length: 651
Score: 578.00 Matches: 108
Percent Similarity: 82.32% Conservative: 27
Best Local Similarity: 65.85% Mismatches: 29
Query Match: 49.11% Indels: 0
DB: 5 Gaps: 0

US-10-690-246a-2 (1-227) x BU994760 (1-651)

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QY 1 MetG1AARG1yVg1leG1u1leYb1leG1uAnPProThrAnAArg1nVal1Thr 20
    |||||
DB 153 ATGGGGGGGGGAAGATCGAGATMAAGGAGATCGAAGACCCACCAAGCAGCGTACC 212
    |||||
QY 21 TysSer1yAARG1yVal1G1y1leu1yVal1a1yVal1u1e1uThrVal1leu1CyAsp 40
    |||||
DB 213 TACTCCAGCGCGGCTCCGGATCATAGAAAGCGCGGAGCTCACCGTCTCTGCGAC 272
    |||||
QY 41 AlAG1nVal1Ser1u1leu1MetPheSer1Thr1y1y1Ser1u1a1Asp1y1r1Cy1Ser1Pro 60
    |||||
DB 273 GCCCAGGTCCGATCATCATGTTCTCTCCACCGCGGCAAGTACCAAGATTCTGCAAGCACC 332
    |||||
QY 61 Ser1Thr1Asp1le1y1le1y1le1y1le1y1r1G1u1A1r1y1r1G1n1Val1Thr1r1G1y1Met1Asp1leu1Trp 80
    |||||
DB 333 GGCACCCACATCAAGGGGATCTTTGACCGCTACCAAGAGGCCATCCGGGACCAAGCTGTGG 392
    |||||
QY 81 Asn1a1aG1n1y1r1G1u1A1r1y1Met1G1n1Asn1Thr1leu1y1b1h1Ser1u1e1nG1u1le1a1nG1n1Asn 100
    |||||
DB 393 ATGACGACAGTATGAAATATGACACCGACCGTACCATCTTCAAGACATCAACAGAGAAC 452
    |||||
QY 101 Leu1A1r1y1Ser1u1le1a1r1G1A1r1y1le1y1le1y1le1y1u1e1u1e1u1G1y1Met1Asp1le1y1Ser1n 120
    |||||
DB 453 CTGGGCAACGAGATCAAGCAAAAGATGGGTGAAGATCTGACCGCGCTCGAGTTCAGAGAG 512
    |||||
QY 121 Leu1A1r1y1leu1G1n1Thr1leu1G1u1Ser1leu1A1r1le1Val1A1r1G1h1a1r1G1y1r1Ty1r 140
    |||||
DB 513 CTGGGGGGCTTGGCAAAATGTCATGCCCTCTCAAGGAGGTTCCCGACAGAGAGTAT 572
    |||||
QY 141 His1Val1le1a1Thr1n1Thr1Asp1Thr1Ty1le1y1Ser1leu1y1Ser1Thr1n1A1r1G1u1Thr 160
    |||||
DB 573 CATGTGATCAACCAAGACTGAACCTTACAGAAAGAGTGAAGCACTCCACAGAGAGCA 632
    |||||
QY 161 Tyr1A1r1G1A1leu1 164
    |||||
DB 633 TACCAAGATCTG 644
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```

RESULT 8
CO997489
LOCUS

DEFINITION
ltu01-6m61-e12 ltu01 lirioidendron tulipifera EST 18-AUG-2004
ltu01-6m61-e12 5', mRNA sequence.

ACCESSION
CO997489
VERSION
CO997489.1 GI:51356713

KEYWORDS
SOURCE

ORGANISM

lirioidendron tulipifera
lirioidendron tulipifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Magnoliales;
Magnoliaceae; lirioidendron.

REFERENCE

1 (bases 1 to 615)
Depamphillis,C., Carlson,J., Ma,H., Soltes,D., Soltes,P.,
Oppenheimer,D., Frohlich,M., Doyle,J., Tankley,S., Webb,M.,
Leedens-Mack,J., Landherr,U., Schlarbaum,S., Ilut,D. and Wall,K.
Generation of ESTs from early flower buds of lirioidendron
tulipifera

TITLE

JOURNAL

COMMENT
Contract: Claude Depamphillis or James Leedens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131

Email: cwid@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (<http://pgn.cornell.edu>)
Plate: ltu01-6m61 row: e column: 12
Seq primer: M13P.

FEATURES

source

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Location/Qualifiers
1..615
/organism="lirioidendron tulipifera"
/mol_type="mRNA"
/db_xref="taxon:3415"
/clone="ltu01-6m61-e12"
/cisue_type="flower buds"
/dev_stage="1-35 mm buds"
/lab_host="SOLR"
/clone_lib="ltu01"
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;  
Site 2: XhoI; This is a directionally cloned,  
non-normalized library. This library has been generated by  
the Floral Genome Project (FGP). The Floral Genome Project  
is funded by NSF's Plant Genome Research Program  
(DBI-0115684). More information about the project can be  
obtained at http://fgp.bio.psu.edu"

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ORIGIN

Alignment Scores:

Pred. No.: 5.96e-58 Length: 615
Score: 576.00 Matches: 110
Percent Similarity: 81.55% Conservative: 27
Best Local Similarity: 65.48% Mismatches: 31
Query Match: 48.94% Indels: 0
DB: 7 Gaps: 0

US-10-690-246a-2 (1-227) x CO997489 (1-615)

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QY 1 MetG1AARG1yVg1leG1u1leYb1leG1uAnPProThrAnAArg1nVal1Thr 20
    |||||
DB 82 ATGGGAAGAGAAAGATAGATTAAGAAAGAAATTCACAGCAAGCAGCAAGTTACA 141
    |||||
QY 21 TysSer1yAARG1yVal1G1y1leu1yVal1a1yVal1u1e1uThrVal1leu1CyAsp 40
    |||||
DB 142 TATTTAAGAGAAAGAGTGGATTTATGAAGAAAGAAAGACTTACCGTCTCTGCGAT 201
    |||||
QY 41 AlAG1nVal1Ser1u1leu1MetPheSer1Thr1y1y1Ser1u1a1Asp1y1r1Cy1Ser1Pro 60
    |||||

```

Db	202	GCAGAGGTTTCTCCATCAGATGTTTCCAGACATCGGAAATTCCTGGAATATTCAGACCCCT	261
Qy	61	SeThrAspIleIysGlyIleTyrGluArgTyrGlnValValInhrGlyMetAspLeuTTP	80
Db	262	TCTCAACACGACGAAAGAAATTTCTGATCGTTTACACGAAATTCACGACAGACCTTATG	321
Qy	81	AsnAlaGlnTyrGluArgMetGlnAsnThrLeuIlyshIstLeuAnGluIleAnGlnAsn	100
Db	322	AACCTCACTACGAGAAATGCAAAATGCACTTGCAACAACTCAAAAGGATTAATACAGT	381
Qy	101	LeuArgIysGluIleArgArgArgIysGlyGluIleuGluIleuGluMetAspIleIysGln	120
Db	382	CTCCGAGGGGAATCAGGCAATAGAGATGGTGAAGATCTGGAGCATCTCGAAATCGAAGAA	441
Qy	121	LeuArgIysLeuGluGlnThrLeuGluGluIserLeuArgIleValAlaGhiIstArgIysTyr	140
Db	442	CTGGCCGGTCTTGAGCAAAATTTTGAAGAGTTCTATCAAAAGTTGTTCCGAAAGAGATAT	501
Qy	141	HisValIleIleAlaThrGlnThrAspThrTyrIleIysIleIysLeuIysSerThrArgGluThr	160
Db	502	CATGTGATCAACACTCAACACGAACTTACAAAGAAAGTTGAGAAACCTTGACAGAAACA	561
Qy	161	TyrArgAlaLeuIleHisGluIleu	168
Db	562	CACGCAATTTTATTCGGGAATTG	585
RESULT 9			
LOCUS	CB971393	762 bp	mRNA linear EST 30-APR-2003
DEFINITION	CAB10005_11a_Fa_B07 Cabernet Sauvignon Flower Pre-bloom - CAB1		
ACCESSION	CB971393		
VERSION	CB971393.1	GI:30254946	
KEYWORDS	EST.		
SOURCE	Vitis vinifera		
ORGANISM	Vitis vinifera		
REFERENCE			
AUTHORS	Goes da Silva,F., Iandolo,A., Lim,H., Baek,J., Leslie,A., Xu,J., Jones,K. and Cook,D.		
TITLE	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contract: Douglas Cook, PhD CARS Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drcocok@ucdavis.edu Seq primer: ACCGACCGACATATGCC. Location/Qualifiers		
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	/mol_type="mRNA"		
	/cultivar="Cabernet Sauvignon"		
	/db_xref="taxon:29760"		
	/clone="CAB10005_11a_Fa_B07"		
	/sex="Hemaphrodite"		
	/dev_stage="Pre-bloom"		
	/lab_host="DH5alpha"		
	/clone_1fb="Cabernet Sauvignon Flower Pre-bloom - CAB1"		
	/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1: SfiI; Site_2: SfiI; CAB1 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and flowers with calyxtraps or caps still attached. Sampled vines were located at the University of California, Davis, Experimental vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in		

cloning as follows:
5'-AAGCAGTGTATCAACGAGAGTGAGCCATTACGGCCGGG-3' and
5'-ATTCTAAGGCGCGAGCGCGCCGATG-dt(30)NN-3'. Library was
constructed using the CloneTech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

Alignment Scores:		1,82e-57	Length:	762
Pred. No.:	Score:	573.00	Matches:	119
Percent Similarity:	Best Local Similarity:	70.22%	Conservative:	39
Query Match:		52.89%	Mismatches:	63
		48.68%	Indels:	4
			Gaps:	4
US-10-690-246A-2 (1-227) x CB971393 (1-762)				
QY	1 MetGlyArgGlyLysIleGluIleLysLysIleGluAsnProThrAsnArgGlnValThr	20		
DB	10 ATGCTGAGAGAAAGATTGAGATCTCAAGAGATGAGAACTCGACGAACAGGCGAGTACC	69		
QY	21 TyrSerLysArgValAlaGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp	40		
DB	70 TACTCCAGAGACCAATATGATATCTTCAAGAAGCCGCTAGGCTCACTGTTCTTGAT	129		
QY	41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspIleCysSerPro	60		
DB	130 GCTAAGGTTTCTATCATCATGCTCTCCAGATCGGAAGCTCCATGAAATCATCAGCCT	189		
QY	61 SerThrAspIleLysGlyIleTyrGlnArgTyrGlnValValThrGlyMetAspLeuTrp	80		
DB	190 TCCACTACAGAAACCAATTTGATTCAGTACAGAACCACTCAGGAGAGGATCTATGG	249		
QY	81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn	100		
DB	250 AGCTATCATCTAGAGAGATTCAGAAACCTGAAAGAACTGAAAGATGTGAACAGAAAT	309		
QY	101 LeuArgLysGluIleArgArgArgLysGlyGlnGluLeuGluGluMetAspIleLysGln	120		
DB	310 CTCAGAGAGAGATTAGGCGAGAGATGGGTAAACATTGAGCCATTGGAGCTTGAGGAA	369		
QY	121 LeuArgGlyLeuGluGlnThrLeuGluGlnLysSerLeuArgIleValAlaGHisArgLysTyr	140		
DB	370 CTGCGAGATCTTGAACCAAGATGAGAGCTTTTGAAGATGTTCTGATAGGAGTAC	429		
QY	141 HisValIleLeuThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr	160		
DB	430 CAGGTGATCAATTAATCAATGGAACCTTCAAGAAAAAGTTAAGAAATGTGGAACAATA	489		
QY	161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluAsnProAsnTyrGlyPheAsn	180		
DB	490 CACAAAAATCTCTCACTAAGATTGTGATCAGAGACAGAGATCAATCAATAGGGCTA---	546		
QY	181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln	200		
DB	547 GTGAGCAATGAGGGGAT---TACGAATCTGTCTGGAATCTCAATGGAAGCTCTCCG	603		
QY	201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGluLysGluTyrGlu	220		
DB	604 GATTATGGCCCTAAGC---TTGAGCCTTAACCGCCTAATGATCTTCACTCGGGGTGGGC	660		
QY	221 SerHisAspLeuSer 225			
DB	661 TCT---GATTGACC 672			
RESULT 10	BU879075	639 bp	mRNA	linear
LOCUS	VO55E10 Populus flower cDNA library Populus balsamifera subsp.			
DEFINITION	trichocarpa cDNA 5 prime, mRNA sequence.			
ACCESSION	BU879075			
VERSION	BU879075.1	GI:24070599		
KEYWORDS	EST.			

SOURCE	Populus balsamifera subsp. trichocarpa (Populus trichocarpa)					
ORGANISM	Populus balsamifera subsp. trichocarpa Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.					
REFERENCE	1 (bases 1 to 639) Umeberg P., Bhalerac R.R., Jansson S. and Sterky F. The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries Unpublished (2002)					
JOURNAL	Contact: BHALERAC RUPALI R. Umea Plant Science Center Department of Plant Physiology University of Umea, 901 87 Umea, Sweden Tel.: +46 90 786 5279 Fax: +46 90 786 6676 Email: rupali.bhalerac@plantphys.umu.se.					
FEATURES	Location/Qualifiers 1..639					
SOURCE	/organism="Populus balsamifera subsp. trichocarpa" /mol_type="mRNA" /sub_species="trichocarpa" /db_xref="taxon:3694" /cfeature_type="floral buds" /clone_lib="Populus flower cDNA library" /note="Organ: flower"					
ORIGIN						
Alignment Scores:						
Pred. No.:	2.84e-57	Length:	639			
Score:	570.50	Matches:	114			
Percent Similarity:	75.94%	Conservative:	28			
Best Local Similarity:	60.96%	Mismatches:	44			
Query Match:	48.47%	Indels:	1			
DB:	5	Gaps:	1			
US-10-690-246A-2 (1-227) x BU879075 (1-639)						
Dn						
Dc						
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Dm						
Dn						
Dc						
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Oy	181 ValGluabengInserArgile 187 : :::
Dd	608 GTGGACAAATGAAGCTGCTGT 628
RESULT 11	
LOCUS	AW737915 698 bp RNA linear EST 18-MAY-2001
DEFINITION	E51333342 tomato flower buds, anthesis; Cornell University
SOURCE	Lycopersicon esculentum CDNA clone CTOD4L21 5', mRNA sequence.
ACCESSION	AW737915
VERSION	AW737915.1 GI:7646860
KEYWORDS	EST.
ORGANISM	Lycopersicon esculentum (tomato)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 698) van der Hoeven,R.S., Bezardes,J.L., Matero,A.L., Holt,I.B., Huang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Rønning,C.M., Niernm,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksey,S.D. Generation of ESTs from tomato flower tissue, anthesis Unpublished (1999) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence. Location/Qualifiers
FEATURES	1..698 /organism="Lycopersicon esculentum" /mol_type="mRNA" /cultivar="TA496" /db_xref="taxon:4081" /clone="CTOD4L21" /tissue_type="flower" /dev_stage="anthesis" /clone_1lb="tomato flower buds, anthesis, Cornell Universily" /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksey; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
ORIGIN	
Alignment Scores:	
Pred. No.:	4.84e-57 Length: 698
Score:	569.00 Matches: 117
Percent Similarity:	69.30% Conservative: 41
Best Local Similarity:	51.32% Mismatches: 64
Query Match:	48.34% Indels: 6
DB:	2 Gaps: 4
US-10-690-246A-2 (1-227) x AW737915 (1-698)	
Oy	2 GlYArGSLyLySiLeGiLuLeLyLYaiLeGuAnProThraAnrGgiNalJnTrTy 21
Dd	3 GGCGTGGAAAAATTGATCATCAAGAAGATTGAACAATCGACAAACAGCAGTCATTAC 62
Oy	22 SerLYaRgArGyValGlylLeLeuLYbLYAlLySiLeUThrValLeuCYaaPaLA 41
Dd	63 TCCAAAGAAAGAAACGGTATTTTCCAAGAAAGCTAAAGAACTTACTGCTCTTGTCAGCGT 122
Oy	42 GlNvaSerLeuLieMetPheSerSerThGLyLYeLeuAlLaApTYrCySeSProSer 61
Dd	123 AAGATCTCTCATCATGCATCATCAAGCACCAAGAGATCATAGATACACAAAGCCCAAC 182
Oy	62 ThrApLiLeLySGLyLeTYrgJuArGYrGlnVaIvalThrGLyMetApLeuTPaAn 81

Db	183	ACTAGCAAAAAGATGATGATGATCATGATCAGAGTCAGCTGGAGTGTATCTGAGC	242
Oy	82	AlaGlnTyrGluArgMetGlnAsnThrLeuIysHisLeuAsnGluLeu	101
Db	243	ATTCACTACGAGAAAATGCAAGAAAATCTGAAGAGATTGAAGAAGATCAATACAGCTA	302
Oy	102	ArgTyrGluIleArgArgTyrLeuGlyGluGluLeuGluGlyMetAspIleLeuGlnLeu	121
Db	303	AGAGAGAGATTAAGCAGAGAACAGGGAGACATGACGGACTTAATATTTTTCAGAGACTA	362
Oy	122	ArgGlyLeuGluGlnThrLeuGluGluGluSerLeuAlaValArgHisArgTyrHis	141
Db	363	TGTCACTTGCAGAGAACATCATCTGAATCTGTCTGAGATTCTGAAAGAAAGTCAAC	422
Oy	142	ValIleAlaThrGlnThrAspThrTyrIleYsIysLeuLeuYsSerThrArgGluThrTyr	161
Db	423	GTGATCAAGAAATCAACAGACACCTCGCAAGAAAGAGGAGAACTTAGAGAGCAAAAT	482
Oy	162	ArgAlaLeuIleHisGluLeuAspMetCysGluGluAsnProAsnTyrGlyPheAsnVal	181
Db	483	GGAAACCTGTGACTTGACTTGGAACCAAAATGTGAAGATCCAAAGATAGTGTT--GTG	539
Oy	182	GluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGlnMet	201
Db	540	GAAATAGAGGGCAAT--TACCACCTGTGTGGCAATTTGGAAATGAGAGTACAAATCTT	596
Oy	202	PheSerPheArgVal-----ValHisProAsnGlnProAsnLeuLeuGlyLeuGlyTyr	219
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Oy	220	GluSerHisAspLeuSerLeuAla	227
Db	654	---TCTCGTACTTACGTCCTCC	674

RESULT 12					
BU877396					
LOCUS	BU877396	605 bp	mRNA	linear	EST 16-OCT-2000
DEFINITION	V033E07 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.				

ACCESSION	BU877396	
VERSION	BU877396.1	GI:24068920
KEYWORDS	EST.	
SOURCE	Populus balsamifera subsp.	trichocarpa
ORGANISM	Populus balsamifera subsp.	trichocarpa

rosids; eucosids I; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 605)
AUTHORS Unmberger, P., Bhalerao, R.R., Jansson, S. and Sterky, P.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
JOURNAL Unpublished (2002)
COMMENT Contact: BHALERAO RUPALI R.

Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel.: +46 90 786 5279
Fax: +46 90 786 6676
Email: ingvald.bhalerao@plantphys.umu.se
Location/Qualifiers

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source
1. 605
/orxaniasm="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"

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ORIGIN	
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Pred. No. :	3.56e-56
Score :	561.00
Length:	605
Matches:	111

Percent Similarity:	76.40%	Conservative:	25
Best Local Similarity:	62.36%	Mismatches:	42
Query Match:	47.66%	Indels:	0
DB:	5	Gaps:	0

US-10-690-246A-2 (1-227) x BU877396 (1-605)

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21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCysAsp 40
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 75 TATCTTCTGAGAGAGAAATGCTCTTTTTCAGAGAGCCAGAGAACTCATCTGACCTTTGTAT 133

41 AlaGlnValSerLeuIleMetPheSerThrGlyLysLeuAlaAspTyrCysSerPro 60
 135 GCTAAGTCTCTCTTTCAGATGTTCTCCACACACAACTAAACAACTCAAGAGATACATTGAGCCCC 19

61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
||| ||| | : : : : ||| | : : : ||| |||
95 TCCACATCGAACAAAGCATTCACGCATCAATTCCAGAACCGTTTAGCGCTAGATCTGTGG 25

81 Asn1agln1yrGluargMetc1asnThrLeuLysHisLeuasnGluileasn1asn 10

Db 255 GGCACTCAATACGAGAAATGCAAGAGCACTTGAGGAAGCTGATGATATCAATCATTAAG 31

Db 315 CTGAGCAGAGAAATCAGGCGAGGAGGAGAGGCGCTGATATGATCTGAGCATTGATCAT 37

Oy 121 LeuArgGlyLeuGlUGInThrleuGlUcIseLLeuArgIleValArghIsArgysTyr 14
| | | | | : | | | | |
Db 375 CTGGCGGTCTTGAGCAACAATGACTGAACCTTTGAATTGGTGTGCCTGGCAGGAAGTAC 43

141 HisValIlealaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 16

Db 435 CATGTCGAAACACAAAACGAAACCTACAGGAGAGAGGCGTGAAGATTTTCAGCGAGAGA 438

Gy 161 TTTArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGly 178

Db 495 CATGAACCTCTTGACGGAATATGAAGCAAACTAGAGATCCACAGTATGGT 548

FEATURE	COORDINATES	ORIENTATION	FEATURE	COORDINATES	ORIENTATION
RESIDUAL	13		CA732396		
LOCUS	CA732396		605 bp	mRNA	Linear
DEFINITION	w11c p005 m21 w11c Triticum aestivum cDNA clone w11c.p005 m21		EST	26-NOV-20	

DEFINITION	MALAC:PHOC.mmal_m2c2c
VERSION	CA732396..1 GI:25547994
ACCESSION	CA732396
	5' end, mRNA sequence.

KEYWORDS	EST.
SOURCE	Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.

REFERENCE
AUTHORS
1 (bases 1 to 605)
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.

TITLE	DuPont Wheat cDNA Sequence
JOURNAL	Unpublished (2002)
COMMENT	Contact: Scott V. Tingey scott.tingey@arsusda.gov

Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2600

Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@USA.dupont.com
 See primer: M13.

FEATURES	Location/Qualifiers
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	/organisms="Triticum aestivum"

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/mol_type="mRNA"

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/db xref="taxon:4565"
/clone="w1pic_pk005.m21"
/tissue_type="lemma and palea"
/lab_host="DH10B"
/clone_lib="w1pic"
/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum, H1 line) lemma and palea"

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ORIGIN

Alignment Scores:

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Score:	557.00	Matches:	105
Percent Similarity:	79.88%	Conservative:	26
Best Local Similarity:	64.02%	Mismatches:	33
Query Match:	47.32%	Indels:	0
DB:	6	Gaps:	0

US-10-690-246A-2 (1-227) x CA732396 (1-605)

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DB 114 ATGGGGGGGGGAGATGATGATTAAGCGGATGAGAACGCCACCAAGCAGGTGACC 173
QY 21 TyrSerLeuArgArgValGlyIleLeuValAlaValGluLeuThrValLeuCysAsp 40
DB 174 TACTCCAGCGCGCGTCCGGGATCATGAAAGGCGCGGAGCTCACCGTCTCGGAC 233
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyValLeuAlaAspTyrCysSerPro 60
DB 234 GCCCAGGTCCCATCATCATCATGTTCTCTCCACCGGCAAGTACCAAGCTTCCAGCAC 293
QY 61 SerThrAspIleLeuGlyIleTyrGlnArgTyrGlnValValThrGlyMetAspLeuTyr 80
DB 294 GGCACCGACATCAAGGGGATCTTTGACCGCTACAGAGCCATCGGAGCACCGCTGTGG 353
QY 81 AsnAlaGlnTyrGlnArgMetGlnAsnThrLeuValHisLeuAsnGlnIleAsnGln 100
DB 354 ATGCAGACAGTATAGATATGATGACGCGCAGCTGAGCATCTCAAGACATCATCGGAC 413
QY 101 LeuArgLyseGluIleArgArgValGlyGluGluGluGluMetAspIleValGln 120
DB 414 CTGCGCAGCCAGATCAGCGCAAGAGATGGTGAAGATGTCGACCGCTCGAGTTCGAGAG 473
QY 121 LeuArgGlyLeuGluGlnThrLeuGluSerLeuArgIleValArgHisArgGlyTyr 140
DB 474 CTGCGGACCTTAAACAAATGTCGATGCCCTCTCAAGAGATCGCCAGNNNAAGTAT 533
QY 141 HisValIleAlaThrGlnThrAspThrTyrLeuValLeuValLeuValSerThrArgGluThr 160
DB 534 CATGTGATCAACGAGGAGACTGAACCTTCAAGAGAGAGTGAAGCACTCCANNAGCA 593
QY 161 TyrArgAlaLeu 164
DB 594 TACAGAGATCTN 605

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RESULT 14

CB972246

692 bp mRNA linear EST 30-APR-2003

DEFINITION

CAB10006_Ia_Fa_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 vitis

ACCESSION

CB972246

VERSION

CB972246.1 GI:30256403

KEYWORDS

EST

SOURCE

vitis vinifera

ORGANISM

vitis vinifera

REFERENCE

Jones, K. and Cook, D. Expressed sequence tags from vitis vinifera 'Cabernet sauvignon' berries at various developmental stages

JOURNAL

Unpublished (2003)

COMMENT

Contact: Douglas Cook, PhD
 CABS Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcook@ucdavis.edu
 Seq primer: ACGTACCGACATATGCC.

FEATURES

source

1..692

Location/Qualifiers

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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10006_Ia_Fa_D07"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom"
/lab_host="DH5alpha"
/clone_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/notes="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1:
SfiI; Site_2: SfiI; CAB1 is a cDNA library of vitis
vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calyptres or caps still attached. Sampled
vines were located at the University of California Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGCAGTGGTATCAACGAGTCGCTATTCAGGCGG-3' and
5'-ATTCTGAGAGCGAGCGCGACATG-dT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

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ORIGIN

Alignment Scores:

Pred. No.:	1.47e-55	Length:	692
Score:	556.50	Matches:	112
Percent Similarity:	70.42%	Conservative:	38
Best Local Similarity:	52.58%	Mismatches:	60
Query Match:	47.28%	Indels:	3
DB:	6	Gaps:	3

US-10-690-246A-2 (1-227) x CB972246 (1-692)

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QY 21 TyrSerLeuArgArgValGlyIleLeuValAlaValGluLeuThrValLeuCysAsp 40
DB 111 TACTCCAGAGAGAAATGATCTTCAAGAGGCGCAGTCACTCATCTTGTGTAT 170
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyValLeuAlaAspTyrCysSerPro 60
DB 171 GCTAAGTTTCTATCATCATGCTCTCCAGTATGAGAAAGCTCAAGAAATCATGAGCCT 230
QY 61 SerThrAspIleLeuGlyIleTyrGlnArgTyrGlnValValThrGlyMetAspLeuTyr 80
DB 231 TCCACTACAACAAATAATTTGATGATGACGAGAACACTCTAGAGATGATCTATGG 290
QY 81 AsnAlaGlnTyrGlnArgMetGlnAsnThrLeuValHisLeuAsnGlnIleAsnGln 100
DB 291 AGCTATCACTATGAGAGATGCAAGAAACCTGAAGAAACTGAAGATGAAACAAGAT 350
QY 101 LeuArgLyseGluIleArgArgValGlyGluGluGluGluMetAspIleValGln 120
DB 351 CTCAGAGAGAGATTTAGCAGAGATGGTGAACATTGAGGATTTAGCGCTTGAAGAA 410
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgGlyTyr 140
DB 411 CTGCGGATCTTGAACAAAGATGAGAGATCTTTGAAGATGTTCTGATAGAAATGAC 470

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 6, 2005, 12:46:31 ; Search time 187 Seconds
(without alignments)
1986.282 Million cell updates/sec

Title: US-10-690-246A-2

Perfect score: 1177
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	51.9	681	3	US-09-410-464-3
2	611	51.9	989	4	US-09-410-464-2
3	496	42.1	989	4	US-09-640-211A-10
4	357.5	30.4	4285	3	US-09-410-464-1
5	354	30.1	905	4	US-09-640-211A-1944
6	344	29.2	386	4	US-09-640-211A-2008
7	341.5	29.0	779	1	US-08-592-214A-9
8	341.5	29.0	779	3	US-08-659-188-9
9	341.5	29.0	779	3	US-08-655-227-9
10	341.5	29.0	779	3	US-08-655-241-9
11	341.5	29.0	779	3	US-09-149-976-9
12	341.5	29.0	779	3	US-09-398-326-9

13	341.5	29.0	779	4	US-09-853-450-9	Sequence 9, Appli
14	326.5	27.7	409	4	US-09-640-211A-1512	Sequence 1512, Ap
15	323	27.4	756	1	US-08-592-214A-11	Sequence 11, Appl
16	323	27.4	756	3	US-08-659-188-11	Sequence 11, Appl
17	323	27.4	756	3	US-08-655-227-11	Sequence 11, Appl
18	323	27.4	756	3	US-08-655-241-11	Sequence 11, Appl
19	323	27.4	756	3	US-09-149-976-11	Sequence 11, Appl
20	323	27.4	756	3	US-09-398-326-11	Sequence 11, Appl
21	323	27.4	756	4	US-09-853-450-11	Sequence 11, Appl
22	322.5	27.4	1159	3	US-09-410-464-14	Sequence 14, Appl
23	322	27.4	714	3	US-09-410-464-15	Sequence 15, Appl
24	320	27.2	756	1	US-08-592-214A-13	Sequence 13, Appl
25	320	27.2	756	3	US-08-659-188-13	Sequence 13, Appl
26	320	27.2	756	3	US-08-655-227-13	Sequence 13, Appl
27	320	27.2	756	3	US-08-655-241-13	Sequence 13, Appl
28	320	27.2	756	3	US-09-149-976-13	Sequence 13, Appl
29	320	27.2	756	3	US-09-398-326-13	Sequence 13, Appl
30	320	27.2	756	4	US-09-853-450-13	Sequence 13, Appl
31	320	27.2	1345	1	US-08-592-214A-7	Sequence 7, Appli
32	320	27.2	1345	3	US-08-659-188-7	Sequence 7, Appli
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36	320	27.2	1345	4	US-09-398-326-7	Sequence 7, Appli
37	320	27.2	1345	4	US-09-853-450-7	Sequence 7, Appli
38	318	27.0	747	4	US-09-853-450-27	Sequence 27, Appl
39	316	26.8	1043	2	US-08-867-087B-12	Sequence 12, Appl
40	316	26.8	1097	1	US-08-460-512-3	Sequence 3, Appli
41	314	26.7	1054	2	US-08-576-156-1	Sequence 1, Appli
42	314	26.7	1057	3	US-08-659-188-1	Sequence 1, Appli
43	314	26.7	1057	3	US-08-655-227-1	Sequence 1, Appli
44	314	26.7	1057	3	US-08-655-241-1	Sequence 1, Appli
45	314	26.7	1057	3	US-09-398-326-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-410-464-3 Application US/09410464
Sequence 3, Appli
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straube et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
EARLIER FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 681
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(681)
US-09-410-464-3

Alignment Scores:
Pred. No.: 5.73e-71
Score: 611.00
Percent Similarity: 70.6%
Best Local Similarity: 51.17%
Query Match: 51.91%
DB: 3
Gaps: 4
US-10-690-246A-2 (1-227) x US-09-410-464-3 (1-681)

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Db 41 GCTAAGGTCTCTTATCATGATGTTCTCCACACATCAACCTCAATGATCAATTAAGCCCC 180
Qy 61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
Db 61 TCCACATCGACAAAGAAATCTACATCAATATCAGAACGCTTAAGCAATAGATCTGTGG 240
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Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
Db 121 CTGCGCGCTTGTAGCAACATATGATCGAAGCCTTGAATGTGTGCGCTGACAGAAATGAC 420
Qy 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
Db 141 CATGTGATCAAAACACAAACGAAACCTACAGAGAAAGTGAAGAAATTTAGAGAGAGA 480
Qy 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrArgLysPheAsn 180
Db 161 CATGAAACCTCTTGTATGATGATATGAAACAAACTAGAGATTCACAGTATGTGTTA--- 537
Qy 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
Db 181 GTGACAAAT-----GAAAGCTGCTGTTCACCTTGAAATGGGGCTTCCAC 582
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Db 201 CTCATCATCTCCGCTGACATCAAGGACCAACACACACACACATCTCCCTAATCTTCCAC 642
Qy 215 LeuGlyLeuGlyTyrGluSerHisAspLeuSerLeu 226
Db 215 CTGGAGATGATTTGGAGCCCATGAACTTGCCCTT 678

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RESULT 2
 US-09-410-464-2
 / Sequence 2, Application US/09410464
 / Patent No. 6335892
 / GENERAL INFORMATION:
 / APPLICANT: Strauss et al.
 / TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 / TITLE OF INVENTION: Poplar and other plant species.
 / FILE REFERENCE: 53375
 / CURRENT APPLICATION NUMBER: US/09/410,464
 / CURRENT FILING DATE: 1999-10-01
 / EARLIER APPLICATION NUMBER: 09/287,700
 / EARLIER FILING DATE: 1999-04-06
 / EARLIER APPLICATION NUMBER: 60/080,851
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 2
 / LENGTH: 946
 / TYPE: DNA
 / ORGANISM: Populus balsamifera subsp. trichocarpa
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)..(684)
 / US-09-410-464-2

Alignment Scores:

Prod. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
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Length: 946	Matches: 128	Conservative: 36	Mismatch: 56	Indels: 12	4
Gaps: 4					

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US-10-690-246a-2 (1-227) x US-09-410-464-2 (1-946)
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Db 1 ATGGGTCTGTGAAAGATTTGAATCAGAAATGCAAAATCCCAACAAACGAGCAAGTACC 60
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Db 21 TACTCGAAGAGAAAGAAATGGTATTTTCAGAAAGCCCAAGAACTCACTGATCTTGTGAT 120
Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
Db 41 GCTAAGGTCTCTTATCATGATGTTCTCCACACATCAACCTCAATGATCAATTAAGCCCC 180
Qy 61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
Db 61 TCCACATCGACAAAGAAATCTACATCAATATCAGAACGCTTAAGCAATAGATCTGTGG 240
Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100
Db 81 GGCACTCAATACGAGAAATGCAAGACACTGAGAGAACTGAAATGATATCAATCAATAG 300
Qy 101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGluMetAspIleLysGln 120
Db 101 CTGAGACAAAGAAATCAGACAGAGAGAGAGAGGCGCTGAAATGATCTGACATTTGATCAT 360
Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
Db 121 CTGCGCGCTTGTAGCAACATATGATCGAAGCCTTGAATGTGTGCGCTGACAGAAATGAC 420
Qy 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
Db 141 CATGTGATCAAAACACAAACGAAACCTACAGAGAAAGTGAAGAAATTTAGAGAGAGA 480
Qy 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrArgLysPheAsn 180
Db 161 CATGAAACCTCTTGTATGATGATATGAAACAAACTAGAGATTCACAGTATGTGTTA--- 537
Qy 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
Db 181 GTGACAAAT-----GAAAGCTGCTGTTCACCTTGAAATGGGGCTTCCAC 582
Qy 201 MetPheSerPheArgValValHisProAsnGln-----ProAsnLeu--- 214
Db 201 CTCATCATCTCCGCTGACATCAAGGACCAACACACACACACATCTCCCTAATCTTCCAC 642
Qy 215 LeuGlyLeuGlyTyrGluSerHisAspLeuSerLeu 226
Db 215 CTGGAGATGATTTGGAGCCCATGAACTTGCCCTT 678

```

RESULT 3
 US-09-640-211A-10
 / Sequence 10, Application US/09640211A
 / Patent No. 6833446
 / GENERAL INFORMATION:
 / APPLICANT: Wood, Marion
 / APPLICANT: Shenk, Michael A.
 / APPLICANT: McGrath, Annette
 / APPLICANT: Glenn, Matthew
 / TITLE OF INVENTION: Compositions and Methods for the
 / TITLE OF INVENTION: Modification of Gene Transcription
 / FILE REFERENCE: 11000.1021C1U
 / CURRENT APPLICATION NUMBER: US/09/640,211A
 / CURRENT FILING DATE: 2000-08-16

```

; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-09-640-211A-10

```

Alignment Scores:

Pred. No.:	1, 6e-55	Length:	989
Score:	496.00	Matches:	110
Percent Similarity:	66.38%	Conservative:	46
Best Local Similarity:	46.81%	Mismatches:	68
Query Match:	42.14%	Indels:	12
		Gaps:	6

US-10-690-246a-2 (1-227) x US-09-640-211A-10 (1-989)

```

QY 1 MetGlyArgGlyLysIleGluIleValLeuValIleGluAsnProThrAsnArgGlnValThr 20
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 ATGGCGAGGGGGAAGATCCAGATCAAGCTATAGAAACAGACGAAACCGGCAAGTGAACC 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 21 TyrSerIleArgArgValGlyIleLeuValGlyAlaValGluLeuThrValLeuCyAsp 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 TACTCGAAGCGGAGGAGGAGGCTTTCAGAAAGCGGAGGAGCTCAGCTTCTAGGCGAC 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCySerPro 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 CCCAAGCTCTTCATCATCATGATATCCAGACCGGCAAGCTCCAGAGTACATCAAGCCCC 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 SerThrAspIleArgGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 TCCAGCTCAAGAAAGAAATGTACATCAGATCAGACGAGCGGCTGAGGTTGATCTCTGG 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 AGCTCTCACTATGAGAAATGCAAGAGAACTGAGAAAGCTGAGAGAGTGAAGTGAACAAG 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluIleMetAspIleValGln 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 307 CTTCAGCTGAGAGTCAAGAGAGAGGTTGCGGGAAGAGATGATGATGATGATGATGATG 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 LeuArgLysLeuGluGlnThrLeuGluGlnSerLeuArgIleValArgHisArgLysTyr 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 TTGGCGGCTTGTGCAAGATGCAACAGCGCTGAGCTGATCCGTCGAAACGGAAGTAC 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleLysLysLeuLysSerThrArgGluThr 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 427 AAGAGCTCGGCAATCAATGACACCGCGGAGAAAGAAAGAAATGCTGAGGAATA 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 161 TyrArgAlaLeuIleHisGlu-----LeuAspMetLysGluGluAsnPro 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 487 AACAAAGTCTTCGCAAGACTGCAACCATTCATCAAGCATCTGAGGAGAGAGACCGG 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 176 AsnTyrGlyPheAsnValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetVal 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 547 CACTTCGGAATG---GTGCAACAC---GCGAGGATTTACGAGGCTGTGATCGGTAATACA 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 196 Asn-----GluCySerProGlnMetPheSerPheArgValAlaHisProAsnGluProAsn 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 GACGCGCGCGCGCGCTGCTGTGACACCTGCGC---CTGCAACCGGACCAAGCCCAT 657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 214 LeuLeu---GlyLeuGlyTyrGluSerHisAspLeuSerLeuAla 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 CTACTACGAGGAGAGATCGGAGAT-CACGACTTACCTTTGCT 701

```

RESULT 4

```

US-09-410-464-1
; Sequence 1, Application us/09410464
; Parent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in

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; TITLE OF INVENTION: Poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4285
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; US-09-410-464-1

```

Alignment Scores:

Pred. No.:	3, 17e-36	Length:	4285
Score:	357.50	Matches:	94
Percent Similarity:	43.65%	Conservative:	16
Best Local Similarity:	37.30%	Mismatches:	29
Query Match:	30.37%	Indels:	113
		Gaps:	3

US-10-690-246a-2 (1-227) x US-09-410-464-1 (1-4285)

```

QY 1 MetGlyArgGlyLysIleGluIleValLeuValIleGluAsnProThrAsnArgGlnValThr 20
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2001 ATGGCGAGGGGGAAGATCCAGATCAAGCTATAGAAACAGACGAAACCGGCAAGTGAACC 2060
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 21 TyrSerIleArgArgValGlyIleLeuValGlyAlaValGluLeuThrValLeuCyAsp 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2061 TACTCGAAGCGGAGGAGGCTTTCAGAAAGCGGAGGAGCTCAGCTTCTAGGCGAC 2120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCySerPro 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2121 GCTAAGTCTCTTATCATGATGTTCTCCACACTAACAACCTGAATGATATAGCCCC 2180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 SerThr-----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2181 TCCACATGACGATACGATACGATCATGTTTCTGCTAAGTATTTCTCGGCTTCTC 2240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 -----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2241 TCTTTCTTTCTTTCTTTCTTTGTTTATGTTGAGTTTATGAACCTTGTAATGCAACC 2300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 -----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2301 GTAGTTTATTTGTTATTTATGACGACGACAAAGAAAGTCTACATCATCATCAAGCG 2360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 IThrGlyMetAspLeuTyrAsnAlaGlnTyrGlu-----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2361 TTTAGGATATGATCTGGGAGCACTCAATACAGGTTAACTTTCTTTCTGCTTTCTT 2420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 -----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2421 CTATATGTTGATCTATAGACGAATATGAGATTTCTCAAGATTTGTTGTTGAGGTTT 2480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 86 -----ArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsnLeuArgLysGly 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2481 GCAGAAATATCAAGAGACATTTGAGGAAGCTGAAATGATCATCATTAAGCTGAGACAGA 2540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 104 uile-----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2541 AATAGTAATCTCAAAAGAAATTAACCTTGCAATATATGATGTATGTTATGTTTATG 2600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 106 -----
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2601 GAATATCTGTAAATTTGTGAGCTACTAATTAAGTATTTGTTTAAACGAGGAGAGA 2660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 109 ysgIyGluGluLeuGluGlyMetAspIleLysGlnLeuArgGlyLeuGluGlnThrLeuG 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2661 GAGAGAGGCGCTGAATGATCTAGACATTAATATCATCTGCGGCTTGAACACATATGA 2720

```

Qy 129 luGluSerLeuArgIleValArgHisArgLys 139
Db 2721 CTGAAGCTTGAAATGATGCTGCGCAGAGAG 2752

RESULT 5
US-09-640-211A-1944
; Sequence 1944, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modifications of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1944
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1944

Alignment Scores:
Pred. No.: 8.01e-37 Length: 905
Score: 354.00 Matches: 80
Percent Similarity: 63.59% Conservative: 44
Best Local Similarity: 41.03% Mismatches: 60
Query Match: 30.08% Indels: 12
Gaps: 6

US-10-690-246a-2 (1-227) x US-09-640-211A-1944 (1-905)

Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLeuAlaAspTyrCysSerPro 60
Db 9 TCCCAATCTTCATCATCATCATCATCTCCAGCAGCGGAACTCCAGCATCATCAGCCCC 68
Qy 61 SerThrAspIleArgGlyIleTyrGluArgTyrGlnValThrGlyMetAspLeuTyr 80
Db 69 TCCACCTCAAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 128
Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuIleIleLeuMetGlnValLeuGln 100
Db 129 AGCTCTCATATGAGAGATGCAAGAGAACCTGAGAACTGAGAGAGGTGAACAGAG 188
Qy 101 LeuArgLysGluIleArgTyrGlyGluGluLeuGluGluMetAspIleTyrGln 120
Db 189 CTTCAAGCTGAGAGTCAAGAGAGAGAGTTCGGGAGAGAGATGATGATGATGATGATG 248
Qy 121 LeuArgLysGluGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
Db 249 TTGGCGGCTTTCGAGCAAGATATGACACAGCCCTTACCTGATCCCTGAAACGAGATAC 308
Qy 141 HisValIleAlaThrArgIleThrAspThrTyrIleIleIleLeuIleSerThrArgGluThr 160
Db 309 AAGAGCTCTGGCAATCAATGACACCGCCAGAAAGAAAGAAAGTCTGAGAAATA 368
Qy 161 TyrArgAlaLeuIleHisGlu-----LeuAspMetLysGluGluAsnPro 175
Db 369 AACAAAGTCTCTCGCAAGACTGCAACCAATCTGATCAAGATCTGAGGAGAGAGACCCG 428
Qy 176 AsnTyrGlyPheAsnValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetVal 195
Db 429 CACTTCGGAATG---GTGCAACAC---GGCAGGATTAACAGAGGTGTGATCGGATATACA 482
Qy 196 Asn-----GluCysProGlnMetPheSerPheArgValValHisProAsnGlnProAsn 213
Db 483 GACGCCGCCGCCGCCGCCGCTGCTGTGTATACACCTGGGC---CTGCAACCGAGACAGCCCAAT 539

Qy 214 LeuLeu---GlyLeuGlyTyrGluSerHisAspLeuSerLeuAla 227
Db 540 CTTACTAGCGGAGAGAGATCGGAGAT-CACGACCTTACCTTGTCT 583

RESULT 6
US-09-640-211A-2008
; Sequence 2008, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modifications of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2008
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2008

Alignment Scores:
Pred. No.: 4.41e-36 Length: 386
Score: 344.00 Matches: 67
Percent Similarity: 74.77% Conservative: 13
Best Local Similarity: 62.62% Mismatches: 27
Query Match: 29.23% Indels: 0
Gaps: 0

US-10-690-246a-2 (1-227) x US-09-640-211A-2008 (1-386)

Qy 1 MetGlyArgGlyValIleGluIleLeuValGluAsnProThrAsnArgGlnValThr 20
Db 61 ATGGGTAGAGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Qy 21 TyrSerLysArgArgValGlyIleLeuLysValAlaLysGluLeuThrValLeuLysAsp 40
Db 121 TACTCAGACGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLeuAlaAspTyrCysSerPro 60
Db 181 GCTAGGTTTTCATCTCTCATGCTCTCCGCAACAGAGCTCCAGAGATCATCAGCCCC 240
Qy 61 SerThrAspIleArgGlyIleTyrGluArgTyrGlnValThrGlyMetAspLeuTyr 80
Db 241 ACCACACAGCAAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuIleIleLeuMetGlnValLeuGln 100
Db 301 ACTACACACTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 101 LeuArgLysGluIleArgArg 107
Db 361 TTTCGAGAGAAATTAAGGCAG 381

RESULT 7
US-08-592-214A-9
; Sequence 9, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

```

STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 10..775
FEATURE:
NAME/KEY: unsure
LOCATION: 778..779
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana CAL"
US-08-592-214A-9

Alignment Scores:
Pred. No.: 2.84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
DB: 1 Gaps: 9

US-10-690-246A-2 (1-227) x US-08-592-214A-9 (1-779)
QY 1 MetGlyArgGlyValIleGluIleValSerIleGluAsnProThrAsnArgGluValThr 20
DB 10 ATGGGAAGGGGTAGGGTTGAATTGAAGAGATAGGAACAAGATCAATAGACAGTGCACA 69
QY 21 TySerIlyAsArgValGlyIleleuIlySylsAlaIySgluLeuThrValIleuCyAsp 40
DB 70 TTCGCAAAAGAAAGACTGCTCTTTGAAGAAAGCTCAGAGATCTCTGTTCTTTGAT 129
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyIlyLeuAlaAspTyrCySerPro 60
DB 130 GCCGAGGTTTCCCTTATGTTCTTCCCATTAAGGCAAAATTGTCGATGACTCCCTGAA 189
QY 61 SerThrAspIleIySglYIle-----TyrGluArgTyrGlnVal----- 73
DB 190 TCTTGATGAGAGAGGTACTGAAAGCCTACGAGAGATTCTTACGCCGAGAGACAGCTG 249
QY 74 -----ValThrGlyMetAspLeuTyrAsnAlaGlnTyrGluArgMet 87
DB 250 ATTGACCTGACTCAGCTTAATGACAGAGCAAGACTGCTGTAATGAGATATGACAGGCTT 309
QY 88 GlnAsnThrLeuIySglIleuIySglIleuIySglIleuIySglIleuIySglIleuIySgl 107

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DB 310 AAGCCAGATTGAG---CTTTGGAGAGAAACAA-----AGGCAT 348
QY 108 ArgIySglYIleGluIleuGluIleuMetAspIleIySglIleuArgIyIleuGluIleuThr 127
DB 349 TATCTGGAGAGAGATTGAAACCAATGACCTCAAGATCTCCAAATCTGGAGCAGCAG 408
QY 128 LeuGluIleuSerIleuArgIleValArgHisArgIySglYIleValIleuIleuThrGlnThr 147
DB 409 CTTGAGACTGCTCTTAAAGCACTTCGCTCCAGAAAAAAATCAACTGATGATAGTCCCTC 468
QY 148 AspThrTyrIlySglYIleuIySglYIleuSerThrArgGluThrTyrArgAlaIleuIleuGlu 167
DB 469 AACCACTCCAAAGAAAGAGAGATACAGAGAGAAACAGACTGCTTACCAAAAC 528
QY 168 LeuAspMetIySglIleuIySglIleuAsnProAsnTyrGlyIyPheAsnValGluIleuIleuSerArgIle 187
DB 529 ATA-----AAGCAGAGGAGAAACATCTTAAGACAAACCAATGCTGAGCAG 579
QY 188 TyrGluAsnSerIleProMetValIleuGluIySglIleuIleuIleuIleuIleuIleuIleu 203
DB 580 CTGACCGGAGCTCGACATGATTAACACAG---CCACAAACATTTCACACACCCCATCTT 636
QY 204 PheArgValIyIleAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 221
DB 637 TACATGATCGCTCATGACACTTCTCTTCTTAATATATGGGTGTTG---TACCAAGA 693
QY 222 HisAsp 223
DB 694 GAAGAC 699

RESULT 8
US-08-659-188-9
Sequence 9, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanoofsky, Martin P.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Plores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 10..775

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Qy 61 SerThcAsp1IeYsg1Yle-----TyrGluArgTyrGlnVal----- 73
Dbb 190 TCTTGATGAGAAAGTACTAGAAAGCTACGAGAGATTTCTTAAGCCGAGAGACAGCTG 249
Qy 74 -----ValThrGlyMetAspLeuTTPsAmIaGlnTyrGluArgMet 87
Dbb 250 ATTGCACCTGACTCTCACCTTAATGACACAGACGAACTGTCATGAGAGATTAGCAGCTT 309
Qy 88 GlnAsnThrLeuYshIstLeuAnGlnIuleAnGlnAneLeuArgYsgIleIeArgArg 107
Dbb 310 AAGGCCAAGATTGAG--CTTTTGAGAGAAACCA-----AGGCAT 348
Qy 108 ArgYsgIYgIuGluIueuGluGluGluMetAsp1IeYsgIuLeuArgYsgIuGlnThr 127
Dbb 349 TATCTGGAGAAAGATTGAGAACCAAGACCTCAAGAGATCTCCAAATCTGGAGACAG 408
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Dbb 469 AACCACTCCAAAGAAAGAGAAAGAGATACAGAGAGAAACAGCATCTTAACAAACAG 528
Qy 168 LeuAspMetYsGluGluAnPProAntYrGlyPheAsnValGluAnGlnSerArgIle 187
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Qy 188 TyrGluAnSerIleProMetValAnGluYsProGlnMetPheSer----- 203
Dbb 580 CTGAACCGCAGCTGACAGATGACACAG--CCACAACCAATTCACACCCCCATCTT 636
Qy 204 PheArgValValHisProAnGlnPro-----AnLeuLeuGlyLeuGlyTyrGluSer 221
Dbb 637 TACATGATCCGCTCATGACACTTCTCTTCTTAATATGAGTGAGTTTG--TACCAAGGA 693
Qy 222 HisAsp 223
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RESULT 10
US-08-655-241-9
Sequence 9, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Weisgel, Deleef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894

```

	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (619) 535-9001	
	TELEFAX: (619) 535-8949	
	INFORMATION FOR SEQ ID NO: 9:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 779 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: double	
	TOPOLOGY: linear	
	MOLECULE TYPE: cDNA	
	FEATURE:	
	NAME/KEY: CDS	
	LOCATION: 10..775	
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	LOCATION: 778..779	
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	FEATURE:	
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	LOCATION: 1..779	
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	US-08-655-241-9	
	Alignment Scores:	
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	Score: 341.50	Matches: 91
	Percent Similarity: 54.13%	Conservative: 40
	Best Local Similarity: 37.60%	Mismatches: 80
	Query Match: 29.01%	Indels: 31
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QY	21 TyrSerLySARGArgVALGIytleLeuLySLySaLaLySGluLeuthrVAlleuCYsAsp 40	
Db	70 TTCTCGAAAAGAAGACTGCTTTTGAGAAAGCTCAGAGATCTCTGTCCTTGTGAT 129	
QY	41 AlaGlnValSerLeuLIemecTheserThrngLyLyLeuAlaAspTyCysserPro 60	
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QY	61 SerThrAspLIeLySGlylle-----TyrGIuArgTYrGlnVal----- 73	
Db	190 TCTTGCAATGAGAGAGTACTTAGAACCTTCAGAGAGTATTTCTTACCCTCAGACACTG 249	
QY	74 -----ValThrGIyMetAspLeuTRPAsnAlaGlnTYrGIuArgmet 87	
Db	250 ATTGCACCTGACTCTCACGTTTATATGACAGACGAACTGGTCATGTAGATGATACAGGCTT 309	
QY	88 GlnAsenThrLeuLyShISleuBengluILeangInAsnLeuArgLySGluILEArg 107	
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QY	108 ArgLySGLIGluGluLeuGluGlyMeTAspLIeLySGlIneuArgLyLeuGluGlnThr 127	
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QY	168 LeuAspMetLySGluGluAnpROAsenTYrGLYPheasnValGIuBengInserArgILE 187	

Dh 529 ATA-----AAGAGAGGAGAAAACATCTTAAGACAAACCAATGTGAGCAG 579
Qy 188 TyGluAmsenSerIleProMetValAengIuCyBProGImetPheSer----- 203
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Qy 204 PheArgValAlHisProAengIuPro-----AsnLeuLeuGlyLeuGlyTyrgIuSer 221
Db 637 TACATGATCGCTCATGACATCTTCTTCTTAATATGAGTGCTTTG---TACCAAGCA 693
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Db 694 GAAGAC 699
RESULT 11
US-09-149-976-9
; Sequence 9, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 779 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..775
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 778..779
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "product = Arabidopsis
; OTHER INFORMATION: thaliana CAL"
US-09-149-976-9
Alignment Scores: 2.84e-35 Length: 779
Pred. No.:

Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
DB: 3 Gaps: 9
US-10-690-246A-2 (1-227) x US-09-149-976-9 (1-779)
Qy 1 MetGlyArgGlyLysIleGluIleLysLysIleGluAenProThrAsnArgGlnValThr 20
Db 10 ATGGGAAGGGGTAGGGTTGATTGAAGAGATTGAAGACAGATCAATGACAGAGACA 69
Qy 21 TySerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
Db 70 TTCTGAAAAGAAAGAACTGCTTTTGAAGAAAGCTCAGAGATCTCTTTGTGAT 129
Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrcySerPro 60
Db 130 GCCGAGTTCCCTTATGCTCTTCTCCCTAAGGCAATGTTGAGACTCTCTGAA 189
Qy 61 SerThrAspIleLysGlyIle-----TyrgIuArgTyrgIuVal----- 73
Db 190 TCTTGATGAGAGAGTACTAGAACGCTAGAGAGATTCTTACGCCGAGACAGACTG 249
Qy 74 -----ValThrGlyMetAspLeuTrpAsnAlaGlnTyrgIuArgMet 87
Db 250 ATTGCACCTGACTCTCAGCTTAATGACACAGAGAACTGGTCAATGAGATATGAGGCTT 309
Qy 88 GlnAenThrLeuLysLeuAengIuIleAengIlnAsnLeuArgLysGluIleArgArg 107
Db 310 AAGGCCAAGATTGAG---CTTTTGGAGAAACCA-----AGGCAT 348
Qy 108 ArgLysGlyGluGluLeuGluIleLysLeuArgIleLysGlnLeuArgGlyLeuGluGlnThr 127
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Qy 128 LeuGluGluSerLeuArgIleValArgHisArgLysTyrgHisValIleAlaThrGlnThr 147
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Qy 148 AspThrTyrgLysLysLeuLysSerThrArgGluThrTyrgAlaLeuIleHisGlu 167
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Qy 168 LeuAspMetLysGluGluAenProAenTyrgIlePheAenValGluAenGlnSerArgIle 187
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Qy 204 PheArgValAlHisProAengIuPro-----AsnLeuLeuGlyLeuGlyTyrgIuSer 221
Db 637 TACATGATCGCTCATGACATCTTCTTCTTAATATGAGTGCTTTG---TACCAAGCA 693
Qy 222 HisAsp 223
Db 694 GAAGAC 699
RESULT 12
US-09-398-326-9
; Sequence 9, Application US/09398326
; Patent No. 6355863
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell and Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

```

STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 10..775
FEATURE:
NAME/KEY: unsure
LOCATION: 778..779
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..779
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana CAL."
US-09-398-326-9

Alignment Scores:
Pred. No.: 2,84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
DB: Gaps: 9

US-10-630-246A-2 (1-227) x US-09-398-326-9 (1-779)
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Db 10 ATGGGAAGGGGTAGGGGTGAATTGAAGAGGATGAGAACAAAGATCAATAGACAAGTGACA 69
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Db 70 TTTCTGAAAAGAGAACTGCTGTCTTTGAAGAAAGCTCAGAGAGATCTCTGTCTTTGTGAT 129
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLybLeuAlaAspTyrCybSerPro 60
Db 130 GCCGAGATTCCCTTATTGCTTCTCTCCCATTAAGGGCAAAATTGTTTCAGATCTCCTCGAA 189
QY 61 SerThrAspIleLybGlyIle-----TyrGluArgTyrGlnVal----- 73
Db 190 TCTTGATGAGAGAAAGTACTAGAACCTGACGAGAGGTATCTTACGCCGAGAGACAGCTG 249
QY 74 -----ValThrGlyMetAspLeuThrAsnAlaGlnTyrGluArgMet 87
Db 250 ATTGACACTGACTCTCAGCTTAATGCACAGACGAACGATGGTCATGAGATNAGCAGGCTT 306

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Qy		88	GlnAsnThrLeuLysHisIleValAsnGluIleLeuAsnGlnAsnLeuArgLysGluIleIleArgArg	107
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Qy		108	ArgLysGIgLIuGLueGluGluIleMetAspIleLysGlnLeuArgGlyLeuGluGlnThr	127
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Qy		128	LeuGluGluSerLeuArgIleValAlaArgHisArgLysTYrHisValIleAlaThrGlnThr	147
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Dz		529	ATN-----AAGAGAGGGAGAAACAATCTTAAGA CA AAA CCAATCATGTCAGAG	576
Qy		188	TYrGluAsnSerIleProMetValAsnGluCysProGlnMetPheSer-----	207
Dz		580	CTGAACCGACGCTCCACGATGTACCAACAG--CCACAACATTTCAACACCCCATTCTT	633
Qy		204	PheArgValValHisProAsnGlnPro-----AsnLeuGluGlyLeuGlyTYrGluSer	223
Dz		637	TACATGATCCCTCATCAGACTTCTCTTCCCAATATAGGGAGGTTC---TACCAAGA	693
Qy		222	HisASP 223	
Dz		694	GAAAGAC 699	
 RESULT 13 US-09-853-450-9 Sequence 9, Application US/09853450 Patent No. 6828478 GENERAL INFORMATION: APPLICANT: Yanoofsky, Martin F. APPLICANT: Pelaz, Soraya APPLICANT: Ditta, Gary TITLE OF INVENTION: The Regents of the University of California TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants FILE REFERENCE: 19452A-002400US CURRENT APPLICATION NUMBER: US/09/853,450 CURRENT FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 61 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 9 LENGTH: 779 TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE: NAME/KEY: CDS LOCATION: (10)..(777) OTHER INFORMATION: CAULIFLOWER (CAL) NAME/KEY: modified base LOCATION: (778)..(779) OTHER INFORMATION: n = g, a, c or t US-09-853-450-9 Alignment Scores: Pred. No.: 2.84e-35 Length: 779 Score: 341.50 Matches: 91 Percent Similarity: 54.13% Conservative: 40 Best Local Similarity: 37.60% Mismatches: 80 Query Match: 29.01% Indels: 31 DB: Gaps: 9 US-10-690-246A-2 (1-227) x US-09-853-450-9 (1-779)				
Qy		1	MetGlyArgGlyLysIleGluIleLysIleValAsnProThrAsnArgGlnValThr	20

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Qy 128 LeuGluGluSerLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 147
Db 409 CTGGAACCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
Qy 148 AspThrTyrLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 167
Db 469 AACCACCTCCAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 528
Qy 168 LeuAspMetLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 187
Db 529 ATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
Qy 188 TyrGluAsnSerLeuProMetValAsnGluCysProGluMetPheSer----- 203
Db 580 CTGACCGCAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
Qy 204 PheArgValValHisProAsnGluPro-----AsnLeuGluGluGluGluGluGlu 221
Db 637 TATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
Qy 222 HisAsp 223
Db 694 GAGAGAC 699

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Alignment Scores:
Pred. No.: 9,89e-34 Length: 409
Score: 326.50 Matches: 70
Percent Similarity: 63.24% Conservative: 16
Best Local Similarity: 51.47% Mismatches: 49
Query Match: 27.74% Indels: 1
DB: 4 Gaps: 1

US-10-690-246a-2 (1-227) x US-09-640-211A-1512 (1-409)
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Qy 87 MetGlnAsnThrLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 106
Db 241 ATGCAAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 300
Qy 107 ArgArgGlyGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 126
Db 301 CAGATATGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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RESULT 15
US-08-592-214A-11
/ Sequence 11, Application US/08592214A
/ Patent No. 5811536
/ GENERAL INFORMATION:
/ APPLICANT: Yanofsky, Martin F.
/ TITLE OF INVENTION: Cauliflower Floral Meristem Identify
/ TITLE OF INVENTION: Genes and Methods of Using Same
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/592,214A
/ FILING DATE: 26-JAN-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-UD 1927
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 756 base pairs

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: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..754
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: NAME/KEY: misc feature
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: OTHER INFORMATION: /note= "product = Brassica oleracea
: OTHER INFORMATION: CAL"
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US-08-592-214A-11
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Pred. No.: 7,53e-33 Length: 756
Score: 323.00 Matches: 83
Percent Similarity: 53.81% Conservative: 37
Best Local Similarity: 37.22% Mismatches: 69
Query Match: 27.44% Indels: 34
DB: 1 Gaps: 6
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US-10-690-246a-2 (1-227) x US-08-592-214A-11 (1-756)

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QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
DB 121 GCTGAGTTTCCCTTATGCTTCTTCCCATAGGGGAAACTGTGAGTACGTCGTGAA 180
QY 61 SerThrAspIleLysGlyIle-----TyrGluArgTyrGlnVal----- 73
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QY 74 -----ValThrGlyMetAspLeuThrPheAlaGlnTyrGluArgMet 87
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QY 88 GlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsnLeuArgLysGluIleArgArg 107
DB 301 AAGGCTAAGATTGAG--CTTTGAGAGAAACCA-----AGGCAT 339
QY 108 ArgLysGlyGluGluLeuGluGlyMetAspIleLysGlnLeuArgGlyLeuGluGlnThr 127
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DB 400 CTGACACTTCTTAAACATATTCGTCGAGAAAAAATCAACTAATGACAGAGTCCCTC 459
QY 148 AspThrTyrLysLysLysLeuLysSerThrArgGluThrTyrArgAlaLeuIleHisGlu 167
DB 460 AACCACTCCAAAGAAAGAGAAAGAAATACCTGAGGAAAAACAGATGCTTCCAAACAG 519
QY 168 LeuAspMetLysGlu-----GluAsnProAsnTyr 177
DB 520 ATAAGCGAGAGAGAGATATCTTAAGACACATCAAAACCAATCAGACAGCAAAACCGC 579
QY 178 GlyPheAsnVal-----GluAsnGlnSerArgIleTyrGluAsnSerIlePro 193
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QY 194 MetValAsn 196
DB 640 TTCTTAAT 648
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Search completed: October 6, 2005, 15:22:14
Job time : 192 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 6, 2005, 13:00:26 ; Search time 711 Seconds
(without alignments)
2223.655 Million cell updates/sec

Title: US-10-690-246a-2

Perfect score: 1177
Sequence: 1 MGRGKIKIKIENPTNRQVT.....HPNQPNLGLGYSHDLSTA 227

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastcap -SUFFIX=p2n.rnpb -MINMATCH=0.1
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Database : Published Applications NA:*

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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1177	100.0	917	20 US-10-690-246-1	Sequence 1, Appli
2	802.5	68.2	1036	20 US-10-690-246-5	Sequence 5, Appli
3	758.5	64.4	980	20 US-10-690-246-7	Sequence 3, Appli
4	755	64.1	898	20 US-10-690-246-7	Sequence 7, Appli
5	675	57.3	681	17 US-10-260-238-5530	Sequence 5530, Ap
6	675	57.3	1257	21 US-10-343-477A-45	Sequence 45, Appli
7	611	51.9	681	14 US-10-104-580-3	Sequence 3, Appli
8	611	51.9	946	14 US-10-104-580-2	Sequence 2, Appli
9	576	48.9	637	21 US-10-487-901-7033	Sequence 7033, Ap
10	557.5	47.4	926	21 US-10-343-477A-49	Sequence 49, Appli
11	556.5	47.3	1036	18 US-10-424-599-120794	Sequence 120794,
12	529.5	45.0	871	18 US-10-425-114-10670	Sequence 10670, A
13	528.5	44.9	644	19 US-10-021-323-8631	Sequence 8631, Ap
14	521.5	44.3	630	21 US-10-487-901-7174	Sequence 7174, Ap
15	509.5	43.3	664	21 US-10-487-901-3483	Sequence 3483, Ap
16	509.5	43.3	665	21 US-10-487-901-7018	Sequence 7018, Ap
17	496	42.1	989	20 US-10-856-499-10	Sequence 10, Appli
18	487.5	41.4	928	19 US-10-437-963-29598	Sequence 29598, A
19	485	41.2	1050	18 US-10-425-114-12758	Sequence 12758, A
20	480	40.8	498	11 US-09-732-627A-4479	Sequence 4479, Ap
21	472	40.1	1155	18 US-10-424-599-66649	Sequence 66649, A
22	471.5	40.1	1231	18 US-10-425-114-15025	Sequence 15025, A
23	462	39.3	1212	18 US-10-425-114-11957	Sequence 11957, A
24	445	37.8	2718	18 US-10-424-599-120795	Sequence 120795,
25	438	37.2	2237	18 US-10-425-114-113190	Sequence 113190, A
26	432	36.7	951	19 US-10-767-795-2121	Sequence 2121, Ap
27	427.5	36.3	639	19 US-10-021-323-86882	Sequence 8682, Ap
28	415	35.3	964	20 US-10-739-930-3300	Sequence 3200, Ap
29	414	35.2	425	11 US-09-922-293-14	Sequence 14, Appli
30	413	35.1	669	19 US-10-021-323-18899	Sequence 8899, Ap
31	413	35.1	1007	18 US-10-425-114-11870	Sequence 14870, A
32	413	35.1	1021	18 US-10-424-599-65326	Sequence 65326, A
33	412	35.0	407	11 US-09-922-293-3394	Sequence 3294, Ap
34	406	34.0	601	19 US-10-021-323-13542	Sequence 13542, A
35	400	34.0	886	15 US-10-278-536-238	Sequence 238, App
36	400	34.0	914	18 US-10-412-699B-55	Sequence 55, Appli
37	399	33.9	632	21 US-10-487-901-3376	Sequence 3376, Ap
38	397	33.7	742	21 US-10-487-901-3474	Sequence 3474, Ap
39	393	33.4	474	11 US-09-732-627A-4667	Sequence 4667, Ap
40	391.5	33.3	674	21 US-10-487-901-3487	Sequence 3487, Ap
41	386	32.8	401	11 US-09-922-293-13	Sequence 13, Appli
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43	386	32.8	904	21 US-10-889-684-3	Sequence 3, Appli
44	385	32.7	780	21 US-10-889-684-4	Sequence 4, Appli
45	382.5	32.5	535	11 US-09-732-627A-3282	Sequence 3282, Ap

ALIGNMENTS

RESULT 1
US-10-690-246-1
Sequence 1, Application US/10690246
Publication No. US20040210967A1
GENERAL INFORMATION:
APPLICANT: CHEN, HONG-HWA
TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
FILE REFERENCE: U 014863-8
CURRENT APPLICATION NUMBER: US/10/690,246
PRIOR FILING DATE: 2003-10-21
PRIOR APPLICATION NUMBER: 091125320
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1

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; LENGTH: 917
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(759)
US-10-690-246-1

Alignment Scores:
Pred. No.: 2,92e-128 Length: 917
Score: 1177.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-690-246a-2 (1-227) x US-10-690-246-1 (1-917)

QY 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgIValThr 20
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Db 76 ATGGGAGGGGGAGATAGAGATTAAGTAAGATTCGACGAACAGCAAGATTACA 135
QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
   |||||
Db 136 TATTCTTAAGAGAGAGATTGGGATATCTGAAGAAGCCCAAGGAGCTACTGTTCTCTGAT 195
QY 41 AlaGluValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCySerPro 60
   |||||
Db 196 GCTCAGGCTCTCTCATCATGTTCTTCAAGCAAGAAAGTTGGCTGATTACTGAGCCCC 255
QY 61 SerThrAspIleLysGlyIleTyrGluArgTyrGluValValThrGlyMetAspLeuTrp 80
   |||||
Db 256 TCTACTGATATTAAGGGGATATATAGAGGATCCAGGTTTGACTGGAATGATCTATAG 315
QY 81 AsnAlaGluTyrGluArgMetGluAsnThrLeuLysIleLeuAsnGluIleAsnGluAsn 100
   |||||
Db 316 AATGCTCATGATATGAGAGATGACAGAAATACCTGAGCATCTGAATGATTAACCAAAAC 375
QY 101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGluMetAspIleLysGlu 120
   |||||
Db 376 CTAGAGGAAGAGATTAAGAGAGAGAGAGAGAGAGAAATTTGAGGAGCATGACATTAAGCAA 435
QY 121 LeuArgGlyLeuGluGluThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
   |||||
Db 436 CTGCGCGGCTTTGAGCAAACTTTGGAAGAGTCTCTTGAAATTTGTTAGGCATTAAGATAT 495
QY 141 HisValIleAlaThrGluThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
   |||||
Db 496 CATGTGATCCGCCACACAACTGACACTTACAGAAAAGCTTAAAGCAACAAGGAAACT 555
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180
   |||||
Db 556 TACCGCGCTTAAATACATGAATCTGATATGAAGAAGAGAAATCCGAATCAGGTTTAAT 615
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCyProGln 200
   |||||
Db 616 GTGAAAACACAGAGTAAATTTATGAAAATTCGATTCGAATGGGATGAGTGTCCACAG 675
QY 201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLysGlyTyrGlu 220
   |||||
Db 676 ATGTTTTCCTTTAGGTTGTTTCAATCCGAATCAGCCCAATCGCTTGGTTTATGAA 735
QY 221 SerHisAspLeuSerLeuAla 227
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Db 736 TCACATGATCTTAGCCTTGCA 756

RESULT 2
US-10-690-246-5
; Sequence 5, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, WEN-CHIEH
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; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (216)..(887)
US-10-690-246-5

Alignment Scores:
Pred. No.: 4,56e-84 Length: 1036
Score: 802.50 Matches: 148
Percent Similarity: 85.90% Conservative: 47
Best Local Similarity: 65.20% Mismatches: 29
Query Match: 68.18% Indels: 3
DB: 20 Gaps: 2

US-10-690-246a-2 (1-227) x US-10-690-246-5 (1-1036)

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QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
   |||||
Db 276 TACTCGAAGAGAGAGCTGCGATTAAGAAAGCGAGGAGATCACTTCTCTCGCAT 335
QY 41 AlaGluValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCySerPro 60
   |||||
Db 336 GCTGAGGTTTCGTTATCATGTTCTTCAAGTACTGGGAAGTTTTCGAGTACTGAGCCCT 395
QY 61 SerThrAspIleLysGlyIleTyrGluArgTyrGluValValThrGlyMetAspLeuTrp 80
   |||||
Db 396 TCAGCGAAGAGAGAGAGGTTTGTGAACCTTCCAGCAGGATCTGGCATTAACCTTGAG 455
QY 81 AsnAlaGluTyrGluArgMetGluAsnThrLeuLysIleLeuAsnGluIleAsnGluAsn 100
   |||||
Db 456 AGCTCCAGTACGAGAGATGCTGATATCGCTTAACCATTCGAAGAGATCAATGCAAT 515
QY 101 LeuArgLysGluIleArgArgArgLysGlyGluGluGluGlyMetAspIleLysGlu 120
   |||||
Db 516 CTGAGGAGGAGATTAAGCAGAGAGATGGGGAAGATCTTGAGGAGACTGATATCAAGGAA 575
QY 121 LeuArgGlyLeuGluGluThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
   |||||
Db 576 CTGCGCGGCTTTGAGAAAACATTAATGAGGATTAAGCTGATGCAATTAAGAAATAT 635
QY 141 HisValIleAlaThrGluThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
   |||||
Db 636 CATGTATACAGTACTAAGCAGACACTTCAAGAAAGATTTGAAGAACTCCCAAGAAACA 695
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180
   |||||
Db 696 CACCGGAATTAATGACGAATTTGGAATCGTTGAGAGACACCAAGTGTATGGGTTCCAC 755
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCyProGln 200
   |||||
Db 756 GAGGATTAAGCAAT-----TATGAGGAGTGTCTTGCTTCAATACAGGCTTCAC 809
QY 201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLysGlyTyrGlu 220
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QY 221 SerHisAspLeuSerLeuAla 227
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Db      867 TCTCAGCATCTGCGCTCGCT 887

RESULT 3
US-10-690-246-3
; Sequence 3, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, MEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 980
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(864)
US-10-690-246-3

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Pred. No.:      6,4e-79      Length:      980
Score:          758.50      Matches:     142
Percent Similarity: 81.94%      Conservative: 44
Best Local Similarity: 62.56%      Mismatches: 36
Query Match:    64.44%      Indels:      5
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US-10-690-246a-2 (1-227) x US-10-690-246-3 (1-980)

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Db      256 TACTCTAAGAGAGAGGCTGGATCATGAAAAAGCGGAGCTCAGCTTCTCTGTGAT 315
QY      41 AlaGlnValSerIleuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
Db      316 GCTCAGCTCTCTCTGTATATGTCTCCAGCACCGGCAAGTTCTCGAGTATTGTACTCT 375
QY      61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
Db      376 ACCACCGATACCAAGAGATGATATGATGTTACCAAGCAGGTGTCGGGCAATAATTATGG 435
QY      81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100
Db      436 AGCAGCAGTACGAGAGATGACAGATACGTTGATCATTTGAAAGAGATTAACCAACCAAC 495
QY      101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGln 120
Db      496 TTGAGAGGAGATTAAGGCAAGATGCGGCAAGATCTTGAAGGGCTTGAAGAAATCAAGAA 555
QY      121 LeuArgLysGluGlnThrLeuGluGlnSerLeuArgIleValArgHisArgLysTyr 140
Db      556 CTGGGTGGTCTTGAAGCAAAATATGAGCAGAGCCCTTAAGCTTGTAAAGATCGAAAGAT 615
QY      141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGlnThr 160
Db      616 CACGTCATCAGACCCAGACAGATACATTCAAAAAAGTTGAAGAACTCTCAAGAAACC 675
QY      161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180
Db      676 CACAGGAACCTTACTCGGAGAGCTG-----GAAACTGACACAGCCGCTTCACTAC 723
QY      181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCyAspProGln 200

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Db      724 GTGAGATGATGCCAAACACTATATGCGCGGCTTGACCTTGAATAATGGGCTTCTAC 783
QY      201 MetPheSerPheArgValAlaHisProAsnGlnProAsnLeuGlyLeuGlyTyrGlu 220
Db      784 TTGATATTCAATTTCGT---ACCCAACCAAGCCAGCCGAACTTCAGGAGATTGATATGTC 840
QY      221 SerHisAspLeuSerIleuAla 227
Db      841 CCTCATGATCTACGTCTCGCC 861

RESULT 4
US-10-690-246-7
; Sequence 7, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, MEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)..(782)
US-10-690-246-7

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Pred. No.:      1,46e-78      Length:      898
Score:          755.00      Matches:     149
Percent Similarity: 82.59%      Conservative: 36
Best Local Similarity: 66.52%      Mismatches: 29
Query Match:    64.15%      Indels:      10
                20          Gaps:      2

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QY      21 TyrSerIysArgArgValGlyIleLeuLysValAlaLysGluLeuThrValIleuCyAsp 40
Db      183 TATTCAAAGAGAGGAGATGATCATGAAAGGAGGATCAAGGAACTCACAGTCTCTGAGAC 242
QY      41 AlaGlnValSerIleuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
Db      243 GCTCAACTCTCATCATCATCTTCTCAAGCTCCGCAAGTTAGTGTATTTCTGACGCCCT 302
QY      61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
Db      303 TCCACAGACCTTAAGATTAAGTATGTTGAGAGGTACCAAAATGTTACCGGAATTGATATATGG 362
QY      81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100
Db      363 GATCGCAATATACAGAGATGCAAGAACCTCTGAGATCTCAGGAGGATTAATCGTAAT 422
QY      101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGln 120
Db      423 CTTCAAGAGAGATTAAGACAGAGAGAGGAGAAATTTGAAAGGTTGGGCGTTAAAGAG 482
QY      121 LeuArgLysGluGlnThrLeuGluGlnSerLeuArgIleValArgHisArgLysTyr 140
Db      483 CTGGCGGTCTTGAAGCAAAATTTGAGAGAGTGGTTAAATTTGTTCCGACAGAAAGTAT 542

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QY 141 HieVal11lea1aThrgInThraPThrTyLyLyLeuLySeuLySeuThraRgJutHr 160
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Db 543 CATGTATCGCTACGCAACACACACTCTTGACAGAAAAGCTCAAAAGCACACACAAATA 602
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QY 161 TTAAGAlaLeu1leHiegluLeuAap--MetLySglu1uAnProAenTyrgLyPhe 179
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|||
Db 603 TACAGAGCCCTTAACGCTGAACTGACAGAACCTGACAGAAATCAACCGTCAGTTT 662
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|||
|||
QY 180 AenValGluAnGlnSerAgi1eTyrgluAnSer1leProMetValaAngluCySPro 199
|||
|||
|||
Db 663 CTGCTGAAAGATCTAAGCTCATCTATGACAGCTCAATTCGAATGCGAAATCGG----- 716
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|||
QY 200 GlnMeCheserPheArGVal1HleProAnGlnProAnLeuGlyLeuGlyTy 219
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QY 220 GluSerHieAap 223
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RESULT 5
US-10-260-238-5530
; Sequence 5530, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katsigiri, Fumiyaaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 5530
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-238-5530

Alignment Scores:
Pred. No.: 2,58e-69 Length: 681
Score: 675.00 Matches: 135
Percent Similarity: 75.11% Conservative: 37
Best Local Similarity: 58.95% Mismatches: 51
Query Match: 57.35% Indels: 6
DB: 17 Gaps: 5

US-10-690-246a-2 (1-227) x US-10-260-238-5530 (1-681)

QY 1 MetG1yArgGlyLy1leGlu1leLy1leGluAnProThraAnAArgInValThr 20
|||
|||
|||
Db 1 ATGGGGCGCGGCAAGATCGAGTCAGATCCAGAAACGCCCAACCCGCGAGTACC 60
|||
|||
|||
QY 21 TyrSerTybAArgVal1Gly1leLeuLybVal1aLySglu1uAnTybVal1leuCyAap 40
|||
|||
|||
Db 61 TACTCCAAAGCGCGGAGGATCATGAAGAGCGCGGAGCTTACCGCTGCGAC 120
|||
|||
|||
QY 41 AlaGlnValSerLeu1leMetPheSerSerThrgLybLeu1aAapTybCySerPro 60
|||
|||
|||
```

```
Db 121 GCCCAGTCGCCATCATCTTCTTCACCGGCAAGTACAGAGTTCTGACCCCC 180
|||
|||
|||
QY 61 SerThraP1leLySgl1leTyrgluAnRgTyrgInVal1aThrgLyMeAapLeuTrp 80
|||
|||
|||
Db 181 GGAACCGACATCAAGACATCTTTGACCGGTCACAGCGCATCGGACCGCTTATG 240
|||
|||
|||
QY 81 Aen1aGlnTyrgluAnRgMetGlnAnThrLeuLybH1eLeuAnGln1leAnGlnAn 100
|||
|||
|||
Db 241 ATCGACAGCTATGAGAAATATGACGCGACGCTGAGACCATCTCAAGACATCAATCGTGT 300
|||
|||
|||
QY 101 LeuAryLySglu1leAryAryLySgl1uGlu1uAnGlu1uMeAap1leLySgl 120
|||
|||
|||
Db 301 CTGCGCACAGCAATTAAGCAAGAGATGGCGAGATCTGGAAGCTTGACTTCAACGAG 360
|||
|||
|||
QY 121 LeuAryGlyLeuGlu1uGlnThrLeuGlu1uSerLeuAry1leValAryH1eAryTy 140
|||
|||
|||
Db 361 CTGCGCGGCTCGAGCAAAAGCTCGACGGGCTCTCAAGAGTTCCCATGGAATAC 420
|||
|||
|||
QY 141 HieVal11lea1aThrgInThraPThrTyLyLyLyLeuLySeuThraRgJutHr 160
|||
|||
|||
Db 421 CATGTATCAGACGACGACGTATACCTTACAAAGAAAAGTGAAGACTCGCACAGCGG 480
|||
|||
|||
QY 161 TTAAGAlaLeu1leHiegluLeuAapMetLySglu1uAnProAnTyrgLyPheAn 180
|||
|||
|||
Db 481 TCAAGAACCTGACAGCAGGACTAGGCAATGCGGAGGAC---CCGCGCTTCGGTAC-- 534
|||
|||
|||
QY 181 ValGluAnGlnSerArg-----1leTyrgluAnSer1leProMetValaAngluCyS 198
|||
|||
|||
Db 535 GTGACACACACGGGCGCGCGCTCGCTTGAGCGGCGCGCGCGCTGCGCGCGG 594
|||
|||
|||
QY 199 ---ProGlnMeCheserPheArGVal1HleProAnGlnProAnLeuGlyLeu 217
|||
|||
|||
Db 595 CGCGCGACATGATGAGCCTTCGCGGTG---CCAGCCAGACCCCACTGACGCGCATG 651
|||
|||
|||
QY 218 GlyTyrgluSerHieAapLeuSerLeu 226
|||
|||
|||
Db 652 GCCTACGCTTCACGACCTCGCGCTG 678
|||
|||
|||
RESULT 6
US-10-343-477A-45
; Sequence 45, Application US/10343477A
; Publication No. US20050066394A1
; GENERAL INFORMATION:
; APPLICANT: Olga Danilevskaya
; APPLICANT: Pedro Hermen
; APPLICANT: Ed Bruggemann
; APPLICANT: David Shitroun
; APPLICANT: Evgenii Ananiev
; APPLICANT: J. Antoni Rafalski
; APPLICANT: Hajime Sakai
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Rebecca B. Cahoon
; APPLICANT: Theodore M. Klein
; TITLE OF INVENTION: Floral Development Genes
; FILE REFERENCE: DD0014-PCT-USR
; CURRENT APPLICATION NUMBER: US/10/343,477A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/253,415
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US01/43750
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Zea mays
US-10-343-477A-45

Alignment Scores:
Pred. No.: 6,32e-69 Length: 1257
Score: 675.00 Matches: 135
Percent Similarity: 75.11% Conservative: 37
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Best Local Similarity: 58.95% Mismatches: 51
 Query Match: 57.35% Indels: 6
 DB: 21 Gaps: 5

US-10-690-246a-2 (1-227) x US-10-343-477A-45 (1-1257)

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QY 1 MetGlyArgGlyValIleGluIleValIleGluAspProThrAsnArgGlnValThr 20
DB 131 ATGGGGCGCGCAAGATCCGAGATCAAGCGGAGAACGCCACCAACCGCCAGGTGACC 190
QY 21 TySerIleArgArgValGlyIleLeuValAlaValSerGluLeuThrValIleuCyasp 40
DB 191 TACTCAAGCGCGCGAGCGGATCATGAAGAAGCGCGCAGCTCACCGCTCTGGGAC 250
QY 41 AlaGlnValSerIleuIleMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
DB 251 GCCAGGTGCGCATCATGTTCTCTCCACCGGCAAGTACACAGAGTCTCAGCCCC 310
QY 61 SerThrAspIleValSerGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
DB 311 GGAACCGACATCAAGACCATCTTGGACCGGTACCAAGAGCCATCGGACCGCTATGG 370
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuValHisLeuAsnGluIleAsnGlnAsn 100
DB 371 ATGAGCAGATATGGAATATGACCGCAACCTGAGCCATCTCAAGACATCATCTGTGT 430
QY 101 LeuArgIleGluIleArgArgArgIleGlyGluIleuGluIleuGluMetAspIleValGln 120
DB 431 CTGGCGCAGAGATATGAGCAAAAGATGGGAGAGATCTGAGCATCTGCACTTGACGAG 450
QY 121 LeuArgIleuGluIleuThrLeuGluIleuSerLeuArgIleValArgHisArgIleVal 140
DB 491 CTGGCGCGCTCGAGCAAAAGCTGACGCGCTCTCAAGAGAGTTCGCCATGAGAACTAC 550
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleValSerLeuValSerThrArgGluThr 160
DB 551 CATGTGATCAGACGACGACATGATACCTTCAAGAAAGAGTGAAGCACTCGCAGAGAGCG 610
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleuAsnProAsnTyrGlyPheAsn 180
DB 611 TACAGAACTCTGACGAGAGAGCTAGGATGGGAGAGAC---CCGGGCTTCGGGTAC--- 664
QY 181 ValGluAsnGlnSerArg-----IleTyrGluAsnSerIleProMetValAsnGluCys 198
DB 665 GTGGCAACACGCGCGCGCGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 724
QY 199 ---ProGlnMetPheSerPheArgValValHisProAsnGlnProAsnLeuGluIleu 217
DB 725 CCGCGGAGATGATGCGCTTCGCGGTGTG---CCAGCGCAGGCCCAACCTGACAGCGCATG 781
QY 218 GlyTyrGluSerHisAspLeuSerIleu 226
DB 782 GCCTACGGCTTCCACGACCTCCGCGCTG 808

```

RESULT 7
 US-10-104-580-3
 ; Sequence 3, Application US/10104580
 ; Publication No. US20030033628A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Straus et al.
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 ; FILE REFERENCE: 62486
 ; CURRENT APPLICATION NUMBER: US/10/104,580
 ; PRIOR FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: 09/410,464
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 09/287,700
 ; PRIOR FILING DATE: 1999-04-06
 ; PRIOR APPLICATION NUMBER: 60/080,851
 ; PRIOR FILING DATE: 1998-04-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 3
 ; LENGTH: 681
 ; TYPE: DNA
 ; ORGANISM: Populus balsamifera subsp. trichocarpa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) .. (681)
 US-10-104-580-3

Alignment Scores:

Pred. No.:	8,92e-62	Length:	681
Score:	611.00	Matches:	128
Percent Similarity:	70.69%	Conservative:	36
Best Local Similarity:	55.17%	Mismatches:	56
Query Match:	51.91%	Indels:	12
DB:	14	Gaps:	4

US-10-690-246a-2 (1-227) x US-10-104-580-3 (1-681)

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QY 1 MetGlyArgGlyValIleGluIleValIleGluAspProThrAsnArgGlnValThr 20
DB 1 ATGGGTGCGAGAAAGATGAAATCAAGAGATCAAAACCCCAACAGCGAGATCAC 60
QY 21 TySerIleArgArgValGlyIleLeuValAlaValSerGluLeuThrValIleuCyasp 40
DB 61 TACTCAAGAGAAAGATGATTTCAAGAAAGCCCAAGAACTCACTGATCTTGAT 120
QY 41 AlaGlnValSerIleuIleMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
DB 121 GCTAAGTCTCTCTTATCATGTTCTCCAACTATMAAACTCAATAGTACATTAGCCCC 180
QY 61 SerThrAspIleValSerGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
DB 181 TCCACATTCAGCAAGAAAGATACGATCAATATCAAGAGCCTTTAGGCATAGTCTGTGG 240
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuValHisLeuAsnGluIleAsnGlnAsn 100
DB 241 GGCATCATATACAGAAATATGCAAGACACTTGAAGAGCTGATATCATATCAATTAAG 300
QY 101 LeuArgIleGluIleArgArgArgIleGlyGluIleuGluIleuGluMetAspIleValGln 120
DB 301 CTGAGCAAGAAATTCAGCGCAGAGAGAGAGAGCGCCTGAATGATCTGACATTTGATCAT 360
QY 121 LeuArgIleuGluIleuThrLeuGluIleuSerLeuArgIleValArgHisArgIleVal 140
DB 361 CTGGCGCGCTCTTGAAGCAATATGACTGAAGCCTTGAATGCTGTGCTGCGAGAGACTAC 420
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleValSerLeuValSerThrArgGluThr 160
DB 421 CATGTGATCAAAACACAAACGAAACCTTACAGAAAGAGTGAAGATTTAGAGAGAGAGA 480
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleuAsnProAsnTyrGlyPheAsn 180
DB 481 CATGGAACCTCTTGATGATGATATGAAGCAAAACTAGAGAGATGACAGATGTGTGTTA--- 537
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
DB 538 GTGGCAAAAT-----GAAGCTGCTGTGGACCTTGCAAAATGGCGCTTCCAAC 582
QY 201 MetPheSerPheArgValValHisProAsnGln-----ProAsnLeu--- 214
DB 583 CTATATCATTCGCGCTGCAATCAAGGACACACACACACATCTTCCTATCTTCAC 642
QY 215 LeuGlyLeuGlyTyrGluSerHisAspLeuSerIleu 226
DB 643 CTTGAGATGATGATTTGAGGCCCAATGAATCTCGCCTT 678

```

RESULT 8
 US-10-104-580-2
 ; Sequence 2, Application US/10104580
 ; Publication No. US20030033628A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Straus et al.

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; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-10-104-580-2

Alignment Scores:
Pred. No.: 1,44e-61 Length: 946
Score: 611.00 Matches: 128
Percent Similarity: 70.69% Conservative: 36
Best Local Similarity: 55.17% Mismatches: 56
Query Match: 51.91% Indels: 12
DB: 14 Gaps: 4

US-10-690-246a-2 (1-227) x US-10-104-580-2 (1-946)
QY 1 MetGlyAArgGlyLyylleGluileLyylleGluAenProThraenAArgGlnValThr 20
   |||||
DB 1 ATGGGTCTGGAGAAAGATTGAATCAAGAAAGATCGAAACCCCAACAGCAAGTCACC 60
   |||||
QY 21 TySerLyAArgArgValGlylleuLyAAlaLyGluLeuThrValLeuCyAap 40
   |||||
DB 61 TACTCGAAGAGAAAGATGATATTTCAGAAAGCCCAAGACCTGACTGACTTTGGAT 120
   |||||
QY 41 AlaGlnValSerleuilewecPheSerSerThrglyLySerleuAlaApyTyCySerPro 60
   |||||
DB 121 GCTAAGTCTCTTTATCATGTTCTCCACACATCAACAAATCATAGATGATTAAGCCC 180
   |||||
QY 61 SerThraPilleLyGlylleTyrgLyAArgGlnValThrGlywecAapLeuTrp 80
   |||||
DB 181 TCCACATCGACAAAGAGATCTACGATCATATCAGAACCGCTTAGCGCATAGATCTGTGG 240
   |||||
QY 81 AenAlaGlnTyrgLyAArgMetGlnAenThrleuLyShleuAenGluileAenGlnAen 100
   |||||
DB 241 GGCATCTCAATGACAAAGAAATGCAAGACCTTAGAGAGAGCTGAAATGATATCAATCATTAG 300
   |||||
QY 101 LeuAryLyGluileAArgAArgLyGlyGluileGluileGlywecApylleYsgln 120
   |||||
DB 301 CTGAGACAGAAATCAAGCAGAGAGAGAGAGGCGCTTGAATGATCTGACATTTGATCAT 360
   |||||
QY 121 LeuAryGlyLeuGluileThrleuGluileGluileSerleuAryGlyleValAryGlyleYr 140
   |||||
DB 361 CTGCGGCGTCTTAGAGCAATATGATGAGAGCTTGAATGATGCTGCGCAGAGATAC 420
   |||||
QY 141 HleValilleAlyThrGlnThrApyThrTyrgLyAlyleuLySerThrApyGluThr 160
   |||||
DB 421 CATGATATCAAAACACAAACGAAACCTTACAGAGAGAGAGGTTGAAGATTGAAGAGAGA 480
   |||||
QY 161 TyAryAlaLeuileHleGluileApyMetLyGluileAenProAenTyrgLyPheAen 180
   |||||
DB 481 CATGAAACCTCTTGATGAAATATGAAGCAAAATAGAGAGATGACAGTATGGTTTAA 537
   |||||
QY 181 ValGluAenGlnSerAryGlyTyrgLyAenSerilleProMetValAenGluCyProGln 200
   |||||
DB 538 GTGAGCAAT-----GAAGCTGCTGTTGACACTTGCAATGGGGCTTCAAC 582
   |||||
QY 201 MetPheSerPheAryValValHleProAenGln-----ProAenLeu--- 214
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DB 583 CTCTATGATTCGGCTGTGATCAAGGAGACACACACACACATCTCTATCTTAC 642
   |||||
QY 215 LeuGlyLeuGlyTyrgLySerHleApyLeuSerleu 226
   |||||
DB 643 CTGGAGATGATTTGAGACCCCATGAACTTCCCTT 678
   |||||

RESULT 9
US-10-487-901-7033
; Sequence 7033, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: Bell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinus, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7033
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7033

Alignment Scores:
Pred. No.: 1.07e-57 Length: 637
Score: 576.00 Matches: 107
Percent Similarity: 84.87% Conservative: 22
Best Local Similarity: 70.39% Mismatches: 23
Query Match: 48.94% Indels: 0
DB: 21 Gaps: 0

US-10-690-246a-2 (1-227) x US-10-487-901-7033 (1-637)
QY 1 MetGlyAArgGlyLyylleGluileLyylleGluAenProThraenAArgGlnValThr 20
   |||||
DB 180 ATGGGAGGGGCAAGATTCAGATCAAGCGGATCGAAGACGCCAACAGCAAGGTGACC 239
   |||||
QY 21 TySerLyAArgArgValGlylleuLyAAlaLyGluLeuThrValLeuCyAap 40
   |||||
DB 240 TACTCGAAGCGCGCACGCGGAGATCATGAAGAGCCAGAGAGCTCACCGTCTTGGCAG 299
   |||||
QY 41 AlaGlnValSerleuilewecPheSerSerThrglyLySerleuAlaApyTyCySerPro 60
   |||||
DB 300 GCCAAGTGCATATCATGTTCTTCTCCACCGGCAAGTACACAGAGTCTGACGCCCT 359
   |||||
QY 61 SerThraPilleLyGlylleTyrgLyAArgGlnValThrGlywecAapLeuTrp 80
   |||||
DB 360 TCCACCGCATCAAGGGAGATCTTTGACCGCTACAGCAAGCAATGCGCACGCCCTTGG 419
   |||||
QY 360 TCCACCGCATCAAGGGAGATCTTTGACCGCTACAGCAAGCAATGCGCACGCCCTTGG 419
   |||||
DB 81 AenAlaGlnTyrgLyAArgMetGlnAenThrleuLyShleuAenGluileAenGlnAen 100
   |||||
DB 420 ATCGACAGATATGAGAAATATGACAGCGCAGCTGAGGACATCTAAGGACATCAACCGCAAC 479
   |||||
QY 101 LeuAryLyGluileAArgAArgLyGlyGluileGluileGlywecApylleYsgln 120
   |||||
DB 480 CTGCGCAGCGAATCAAGCAGAAAGATGAGAGAAATCTGAGCGGCTGAGTTCGACGAG 539
   |||||
QY 121 LeuAryGlyLeuGluileThrleuGluileGluileSerleuAryGlyleValAryGlyleYr 140
   |||||
```

Db 540 CTGCGGCTCTTGAGCAAAATGTCGATGCCGCTCAAGAGGTTGCCACAGGAATAT 599

Qy 141 HisvalIleAlaThrGlnThrAspThrTyrlslyls 152
Db 600 CATGTGATCAGCACACAGACTGAACCTTCAAGAAA 635

RESULT 10
US-10-343-477A-49
; Sequence 49, Application US/10343477A
; Publication No. US2005006394A1
; GENERAL INFORMATION:
; APPLICANT: Olga Danilevskaya
; APPLICANT: Pedro Hermon
; APPLICANT: Ed Bruggemann
; APPLICANT: David Shitroun
; APPLICANT: Evgenii Ananiev
; APPLICANT: J. Antoni Rafaleki
; APPLICANT: Hajime Sakai
; APPLICANT: Bogar B. Caloon
; APPLICANT: Rebecca E. Klehn
; APPLICANT: Theodore M. Klein
; TITLE OF INVENTION: Floral Development Genes
; FILE REFERENCE: DD0014-PCT-USR
; CURRENT APPLICATION NUMBER: US/10/343,477A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/253,415
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US01/43750
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Glycine max
US-10-343-477A-49

Alignment Scores:
Pred. No.: 2.8e-55 Length: 926
Score: 557.50 Matches: 109
Percent Similarity: 70.89% Conservative: 42
Best Local Similarity: 51.17% Mismatches: 59
Query Match: 47.37% Indels: 3
Gaps: 3

US-10-690-246a-2 (1-227) x US-10-343-477A-49 (1-926)

Qy 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgIleValThr 20
Db 11 ATGCTGAGAGAAAGATCCAGATCAGATCAGATCAGAAACAAACCAACCGCAGGTCACT 70

Qy 21 TySerIysArgValGlyIleLysIleLysValAlaLysGluLeuThrValLeuCysAsp 40
Db 71 TACTCTAAACGACGGAATGCGCTTTCAAGAGGCCAAACGAGCTTACCGTTCTCTCGCAT 130

Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrcysSerPro 60
Db 131 GCCAAGTTTCTATTATTATTATGTTCTCCAGCAGCTGGAACCTCCACAGATCATCAGCCCC 190

Qy 61 SerThrAspIleLysGlyIleTyrgLysArgTyrgIleValValIleThrGlyMetAspLeuTrp 80
Db 191 TCCACCTCAACAAAGAGTTCTTCGATCAATACAGATGACTCTGGGAGTTGATCTCTGG 250

Qy 81 AsnAlaGlnTyrgLysArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100
Db 251 AACCTCATTTACGAGATATCCAGACAACTTGAAGAACTGAAGAGGTAAATAGCAAT 310

Qy 101 LeuArgLysGluIleArgArgArgLysGlyGluLysGluLysGluMetAspIleLysGln 120
Db 311 CTTGTAAAGAGATTAGGCAAGAAATGGAGATGTCGAACGAGCTGGCATGGAGAAAT 370

Qy 121 LeuArgLysGluIleArgArgArgLysGlyGluLysGluLysGluMetAspIleLysGln 140
Db 121 LeuArgLysGluIleArgArgArgLysGlyGluLysGluLysGluMetAspIleLysGln 140

Db 371 CTCAGGCTCTTGAGGAAGAAATGGAACAGCCCGCAAGTTGTTGTCGAGCGTAAGTAT 430

Qy 141 HisvalIleAlaThrGlnThrAspThrTyrlslylslylsLysSerThrArgIleThr 160
Db 431 AAGGTGATTAACAATCAGATTGACACCCAGGAAAAAGTTTAATTAACAGAAAGAAAGTG 490

Qy 161 TyArgAlaLeuIleHisGluLeuAspMetLysGluLysProAsnTyrgIlePheAsn 180
Db 491 CACACAGGCTCTCTGATATGATTCGATGCAAAAGCAAGATCCACGTTTGATTCGATTCG 547

Qy 181 ValGluAsnGlnSerArgIleTyrgLysAsnSerIlePrometValAsnGluCysProGln 200
Db 548 ATAGATTAATGAGAGGGAG--TATGAGTCTGATCGATTCGAAATTTAGGTCCAGCC 604

Qy 201 MetPheSerPheArgValValHisProAsnGlnProAsn 213
Db 605 ATGTTGCAATTGAGC---ATACAAACCAACCAATCTTAGT 640

RESULT 11
US-10-424-599-120794
; Sequence 120794, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120794
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURK:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1
US-10-424-599-120794

Alignment Scores:
Pred. No.: 4.34e-55 Length: 1036
Score: 556.50 Matches: 108
Percent Similarity: 71.36% Conservative: 44
Best Local Similarity: 50.70% Mismatches: 58
Query Match: 47.28% Indels: 3
Gaps: 3

US-10-690-246a-2 (1-227) x US-10-424-599-120794 (1-1036)

Qy 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgIleValThr 20
Db 27 ATGCTGAGAGAAAGATCCAGATCAGATGAGATGAGAACACCAACCCCGCAGGTCACT 86

Qy 21 TySerIysArgValGlyIleLysIleLysValAlaLysGluLeuThrValLeuCysAsp 40
Db 87 TATTCTAAAGACGAGATGCGCTTTCAAGAGGCCAAACGAGCTCAACGTTCTATGCGAT 146

Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrcysSerPro 60
Db 147 GCCAAGTTTCTATTATTATTATGTTCTCCAGCAGCTGGAACTCCACAGATCATCAGCCCC 206

Qy 61 SerThrAspIleLysGlyIleTyrgLysArgTyrgIleValValIleThrGlyMetAspLeuTrp 80
Db 207 TCCACCTCAACAAAGAGCTTCTTCGATCAGATCAGATGACTCTAGGAGTCTCTCTGG 266

Qy 81 AsnAlaGlnTyrgLysArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100
Db 267 AACCTCATTTACGAGATTAATGCAAGAACCTTGAAGAACTGAAGAGGTAAATAGCAAT 326

Qy 101 LeuArgLysGluIleArgArgArgLysGlyGluLysGluLysGluMetAspIleLysGln 120
Db 101 LeuArgLysGluIleArgArgArgLysGlyGluLysGluLysGluMetAspIleLysGln 120

Db 327 CTTCGTAAGAGATTAGGACGATGGAGATTGCTGTAAGCATCTGGCATGGAAGAT 386
 QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgGlyTyr 140
 Db 387 CTCACACTCTTGAAGAGAAATGACACAGCCGCAAGGTTGTGTGAGCGTAAGTAT 446
 QY 141 HisValIleAlaThrGlnThrAspThrTyrTyrLeuLeuLeuLeuSerThrArgGluThr 160
 Db 447 MAGGTATTAACAATACGATGACACCCACAGGAAAAGTTTAACTAACGAAAGAGT 506
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluGluAsnProAsnTyrGlyPheAsn 180
 Db 507 CACACAGACTCTGATGACTTGGATGACAAAGCAGAAAGATCCAGTTTGCAATG 563
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
 Db 564 ATGATTAATGAGAGGGAG--TACGAGTCTGTGATGGATTCTCAAAATTAAGTCCAGC 620
 QY 201 MetPheSerPheArgValValHisProAsnGlnProAsn 213
 Db 621 ATGTTGCAATTGAGC--CTACAGCCCAAGCATCTTAGT 656

RESULT 12
 US-10-425-114-10670
 ; Sequence 10670, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaka, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 10670
 ; LENGTH: 871
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700958586_FLI
 ; US-10-425-114-10670

Alignment Scores:
 Pred. No.: 5,1e-52 Length: 871
 Score: 529.50 Matches: 103
 Percent Similarity: 70.81% Conservative: 45
 Best Local Similarity: 49.28% Mismatches: 58
 Query Match: 44.99% Indels: 3
 DB: 18 Gaps: 3

US-10-690-246a-2 (1-227) x US-10-425-114-10670 (1-871)

QY 5 LysIleGluIleuLysIleGluAsnProThrAsnArgGlnValThrTyrSerLysArg 24
 Db 3 AAGATCCAGATCAAGAGATGAGAACACACCAACCGCAGGTCTTATTTCTAAACGA 62
 QY 25 ArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuGlyAspAlaGlnValSer 44
 Db 63 CGGAATGGCTTTTCAAGAAAGCCACAGACTCACCTTCTATAGCGATGCCAAGTTTCT 122
 QY 45 LeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerProSerThrAspIle 64
 Db 123 ATATTATGTTCTCCAGACCTGGGAAACTCCAGAGATACATACGCCCTCCACTCAACA 182
 QY 65 LysGlyIleTyrGluArgGlyGlnValValThrGlyMetAspLeuThrAsnAlaGlnTyr 84
 Db 183 AAGCAGTTCTTCGATCAGTACCAAGATGATCTGAGAGTCAATCTCTGAACTCTCATAC 242

QY 85 GluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsnLeuArgLysGlu 104
 Db 243 GAGATATGCAAGAGAACTTGAAGAACTCAAGAGATGGAATCTTCGTAGGAG 302
 QY 105 IleArgArgArgLysGlyGluGluGluGluGluMetAspIleLysGlnLeuArgGlyLeu 124
 Db 303 ATTAGGACAGGATGGGAGATGCTGAAACGATCTGGCAGTCAGGAATCTCAAGCTCTT 362
 QY 125 GlnGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyrHisValIleAla 144
 Db 363 GAGAAAGAAATGACAAAGGCCCCAGAGTTGTCTGAACTGAATTAAGTGTAACTA 422
 QY 145 ThrGlnThrAspThrTyrTyrLeuLysLeuLysSerThrArgGluThrTyrArgAlaLeu 164
 Db 423 ATTCGATTGACACCCAAAGGAAAAGTTTAACTAACGAAAGATGACACACGACTC 482
 QY 165 IleHisGluLeuAspMetLeuGluGluAsnProAsnTyrGlyPheAsnValGluAsnGln 184
 Db 483 CTGCGGCACTTGATGACCAAGACAGACAGATCCACCTTTTGCAATG--ATAGATATGGA 539
 QY 185 SerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGlnMetPheSerPhe 204
 Db 540 GGGGAG--TACGAGTCTGTGATCGGATTTCTCAAAATTAAGTCCACGCAATGTCGAT 596
 QY 205 ArgValValHisProAsnGlnProAsn 213
 Db 597 AGC--CTACAGCCCAAGCATCTTAGT 620

RESULT 13
 US-10-021-323-8631
 ; Sequence 8631, Application US/10021323
 ; Publication No. US20040123340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dekman, Jill
 ; APPLICANT: Feng, Paul C.C.
 ; APPLICANT: Fincher, Karen L.
 ; APPLICANT: Ziegler, Todd E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(52274)B
 ; CURRENT APPLICATION NUMBER: US/10/021,323
 ; CURRENT FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: US 60/255, 619
 ; PRIOR FILING DATE: 2000-12-14
 ; NUMBER OF SEQ ID NOS: 17880
 ; SEQ ID NO 8631
 ; LENGTH: 644
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(644)
 ; OTHER INFORMATION: unsure at all n locations
 ; OTHER INFORMATION: Clone ID: LIB3828-013-01-K6-F12
 ; US-10-021-323-8631

Alignment Scores:
 Pred. No.: 4.3e-52 Length: 644
 Score: 528.50 Matches: 108
 Percent Similarity: 71.84% Conservative: 40
 Best Local Similarity: 52.43% Mismatches: 56
 Query Match: 44.90% Indels: 3
 DB: 19 Gaps: 2

US-10-690-246a-2 (1-227) x US-10-021-323-8631 (1-644)

QY 1 MetGlyArgGlyLysIleGluIleuLysLysIleGluAsnProThrAsnArgGlnValThr 20
 Db 32 ATGGCTCGAGGAGAAAGTCAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 91
 QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuGlyAsp 40
 Db 92 TATTGAAAGAGAAACGCTCTTTCAAGAAAGCTAATGAATTAAGTCTTTCGAT 151

Qy	41	AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro	60
Db	152	GCTAAGTTTGCATCATCATGTTTTCCACTACTGGTAACTCCAAAGATTATCAGCCCT	211
Qy	61	SerThrAspIleIleGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp	80
Db	212	TCCACCCAAACGAAAGCAGTAAATGATCAGTACCAAGAAACCTTGGGGATGAAATCTGG	271
Qy	81	AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn	100
Db	272	AAACACCCACTATGAGAAATATGCAGAGCAGTTGAAGACGCTGAAGAGGTTAAACAGAAC	331
Qy	101	LeuArgLysGluIleLeuArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGln	120
Db	332	CTGGCGAAAGAGATTAGAGAAAGATGGGCACTGTTGAAATGATTTGACATCAAGAAAT	391
Qy	121	LeuArgGlyLeuGluGlnThrLeuGluLysSerLeuArgIleValArgHisArgLysTyr	140
Db	392	CTTGCTGCTTTGGAAACAGAAATGAGAGCTCTGCACTTATTCGTGATGAGAAAGAT	451
Qy	141	HisValIleLeuAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr	160
Db	452	CGTGTCTCTCCAAACCAATCGATCGATCTTCCAGAAAGAGTAGAGAAATGGAAGATA	511
Qy	161	TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn	180
Db	512	CACAAAAATCTCTTACATGAACTGAATCCCTGGAAGAAAGATCCA--TATGGAATTA--	566
Qy	181	ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln	200
Db	567	GTTGATTAATGAGGGGAT--TATGATACCTGATCGGGTATCAAAATGAGAGTCTCGT	623
Qy	201	MetPheSerPheArgVal	206
Db	624	ATATTGCTTTAAGCCTG	641

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RESULT 14
US-10-487-901-7174
; Sequence 7174, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thadeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinus, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 7174
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7174

Alignment Scores:
Pred. No.: 2.78e-51 Length: 630
Score: 521.50 Matches: 99
Percent Similarity: 70.65% Conservative: 43
Best Local Similarity: 49.25% Mismatches: 56
Query Match: 44.31% Indels: 3

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DB:	21	Gaps:	1
US-10-690-246A-2	(1-227)	x	US-10-487-901-7174 (1-630)
QY	1	MetGlyArgGlyLysIleGluIleLysLysIleGluAsnProThrAsnArgGlnValThr	20
DB	34	ATGGCTGCTGGGAAGATCCAGATCAAGAGATAGAGAACCAACAAACAGACAACTCACT	93
QY	21	TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCysAsp	40
DB	94	TATCTAAGAAAGAAATGAGACTTTTCAAGAAAGCAAAATGAACCTCACTGTTCTTGCTGAT	153
QY	41	AlaGlnValSerLeuIleMetPheSerSerThrGlyLysPheAlaAspTyrCysSerPro	60
DB	154	GCTAAAGTTCTATATATATATATATTTCAAGTACAGAAAACCTTCATGAATTTTAAGCTCT	213
QY	61	SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp	80
DB	214	TCTGCACAGCACCAAGCACTTGTTCATCTGTATCAAAAGACCTGTGAGTTGATCTTTCG	273
QY	81	AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn	100
DB	274	AACTCCCACTATGAAATAATGACAAAGCAGTTGAGAAAGCTAAAGATGTATATAGCAAT	333
QY	101	LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGluMetCysAspIleLysGln	120
DB	334	CTCCGAAAGAGATCAGGCAGAGATGGAGAAAGCAAAAGATCTTGAACTATATGAGCAG	393
QY	121	LeuArgGlyLeuGluGlnThrLeuGluGluGluSerLeuArgIleValArgHisArgLysTyr	140
DB	394	TTGGAAAGCTCAATGAATAATGTGACAATTTCTGAAAGCTTATTTCTGAAAGAACTAT	453
QY	141	HisValIleLeaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr	160
DB	454	AAAGGATTTAGCAATCAAGATTGAAACGTACAAAGAAAGAGCTCGGAAATGTGAAAGAAATA	513
QY	161	TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn	180
DB	514	CATGAATAATCTCTGCTTGAATTTGATGCAAGAAAGAAAGAAAGCA-----TATGGA	564
QY	181	ValGluAsnGlnSerArgLysTyrGluAsnSerIleProMetValAsnGluCysProGln	200
DB	565	TTGCTTGAAGCAAGAAAGGAGCTATATATCTGTGCTTGATTTCCCAATATGAGGCGCACGC	624
QY	201	Met	201
DB	625	ATA	627

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RESULT 15
US-10-487-901-3483
; Sequence 3483, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrina, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3483
; LENGTH: 664
; TYPE: DNA
;

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